

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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1  TGGCAGTGGG CGGCGTAGAG CACTGCAGCA GCAATGACGG AGGGCACGTG
51 TCTGCGGCGC CGAGGGGGCC CCTACAAGAC CGAGCCCGCC ACCGACCTCG
101 GCCGCTGGCG ACTCAACTGC GAGAGGGGCC GGCAGACGTG GACCTACCTG
151 CAGGACGAGC GCGCCGGCCG CGAGCAGACC GGCCTGGAAG CCTACGCCCT
201 GGGGCTGGAC ACCAAGAATT ACTTTAAGGA CTTGCCCAAA GCCCACACCG
251 CTTTGTAGGG GGCTCTGAAC GGGATGACAT TTTACGTGGG GCTGCAGGCT
301 GAGGATGGGC ACTGGACGGG TGATTATGGT GGCCCACTTT TCCTCCTGCC
351 AGGCCTCCTG ATCACTTGCC ACGTGGCAGC CATCCCTCTG CCAGCCGGAT
401 ACAGAGAAGA GATTGTGCGG TACCTGCGGC ACATTGAGGA TAAGTCCACC
451 GTGTTTGGGA CTGCGCTCAA CTATGTGTCT CTCAGAATTC TGGGTGTTGG
501 GCCTGACGAT CCTGACCTGG TACGAGCCCG GAACATTCTT CACAAGAAAG
551 GTGGTGTGTT GGCCATCCCC TCCTGGGGGA AGTTCTGGCT GGCTGTCCTG
601 AATGTTTACA GCTGGGAAGG CCTCAATACC CTGTTCCCAG AGATGTGGCT
651 GTTTCCTGAC TGGGCACCGG CACACCCCTC CACACTCTGG TGCCACTGCC
701 GGCAGGTGTA CCTGCCCATG AGCTACTGCT ACGCCGTTCG GCTGAGTGCC
751 GCGGAAGACC CGCTGGTCCA GAGCCTCCGC CAGGAGCTCT ATGTGGAGGA
801 CTTCGCCAGC ATTGACTGGC TGGCGCAGAG GAACAACGTG GCCCCGACG
851 AGCTGTACAC GCCGCACAGC TGGCTGTCTC GCGTGGTATA TGCGCTCCTC
901 AACCTGTATG AGCACCACCA CAGTGGCCAC CTGCGGCAGC GGGCCGTGCA
951 GAAGCTGTAT GAACACATTG TGGCCGACGA CCGATTACAC AAGAGCATCA
1001 GCATCGGCCC GATCTCGAAA ACCATCAACA TGCTTGTGCG CTGGTATGTG
1051 GACGGGCCCG CCTCCACTGC CTTCCAGGAG CATGTCCTCA GAATCCCGGA
1101 CTATCTCTGG ATGGGCCTTG ACGGCATGAA AATGCAGGGC ACCAACGGCT
1151 CACAGATCTG GGACACCGCA TTCGCCATGC AGGCTCTGCT TGAGGCGGGC
1201 GGGCACCACA GGCCCGAGTT TTCGTCTGCT CTGCAGAAGG CTCATGAGTT
1251 CCTGAGGCTC TCACAGGTCC CAGATAACCC TCCCGACTAC CAGAAGTACT
1301 ACCGCCAGAT GCGCAAGGGT GGCTTCTCCT TCAGTACGCT GGACTGCGGC
1351 TGGATCGTTT CTGACTGCAC GGCTGAGGCC TTGAAGGCTG TGCTGCTCCT
1401 GCAGGAGAAG TGTCCTCCATG TCACCAGCA CATCCCCAGA GAACGGCTCT
1451 GCGATGCTGT GGCTGTGCTG CTGAACATGA GAAATCCAGA TGGAGGGTTC
1501 GCCACCTATG AGACAAGCG TGGGGGGCAC TTGCTGGAGC TGCTGAACCC
1551 CTCGGAGGTC TTCCGGGACA TCATGATTGA CTACACCTAT GTGGAGTGCA
1601 CCTCAGCCGT GATGCAGGCG CTTAAGTATT TCCACAAGCG TTTCCCGGAG
1651 CACAGGGCAG CGGAGATCCG GGAGACCCCTC ACGCAGGGCT TAGAGTTCTG
1701 TCGGCGGCAG CAGAGGGCCG ATGGCTCCTG GGAAGGCTCC TGGGGAGTTT
1751 GCTTCACCTA CGGCACCTGG TTTGGCCTGG AGGCCTTCGC CTGTATGGGG
1801 CAGACCTACC GAGATGGGAC TGCCGTGTGA GAGGTCTCCC GGGCCTGTGA
1851 CTTCCCTGCT TCCCGGAGA TGGCAGACGG AGGCTGGGGG GAGGACTTTG
1901 AGTCCTGCGA GGAGCGGCGT TATGTGCAGA GTGCCCAGTC CCAGATCCAC
1951 AACACATGCT GGGCCATGAT GGGGCTGATG GCCGTTCGGC ATCCTGACAT
2001 CGAGGCCCAG GAGAGAGGAG TCCGGTGTCT ACTTGAGAAA CAGCTCCCCA
2051 ATGGCGACTG GCCGCAGGAA AACATTGCTG GGGTCTTCAA CAAGTCTCTG
2101 GCCATCTCCT ACACGAGCTA CAGGAACATC TTCCCCATCT GGGCCCTCGG
2151 CCGCTTCTCC CAGCTGTACC CTGAGAGAGC CCTTGCTGGC CACCCCTGAG
2201 AACATGCCTA CCTGCTGGGT GCCGTCTGTG CGTTCAGTG AGGCCAAGGG
2251 GTCCTGGCCG GGTGGGGAG CCCTCCCATG ACCCTGTCTT GGGCTCCAAC
2301 CCCTCAACCT CTATCTCATA GATGTGAATC TGGGGGCCAG GCTGGAGGCA
2351 GGGATGGGGA CAGGTGAGGT GGCTTAGACT CTTGATTTT ACTGTAGGTT
2401 CATTTCGAA AGTAGCTTGT CGGGCTTGGG TGAGGAAGGG GGCACAGGAG
2451 CCGTGACCCC TGAGGAGGCA CAGCGCCTTC TGCCACCTCT GGGCACGGCC
2501 TCAAGGTAGT GAGGCTAGGA GGTTTTCTCT GACCAATAGC TGAGTTCTTG
2551 GGAGAGGAGC AGCTGTGCCT GTGTGATTCC TTAGTGTCGA GTGGGCTCTG
2601 GGCTGGGGTC GGCCCTGGGC AGGCTTCTCC TGCACCTTT GTCTGCTGGG
2651 CTGAGGGACA CGAGGGCAAC CCTGTGACAA TGGCAGGTAG TGTGCATCCG
2701 TGAATAGCCC AGTGCGGGG TTGCTCATGG AGCATCCTGA GGCCGTGCAG
2751 CAGGGAGCCC CATGCCCTG GGTCTGTAGC TTGCTGCGT ATGGGGTGGT
2801 GTCATGGAGC CTCATGCCCT TGGGTCGTGA GCTCGCCTGA GTATGGGGTG
2851 GTGTCAAGGA GCCGCATACC CCTGGGTGTT GAGCTCGCTG GCATATGCAG
2901 GGTCTGTCTG GGAACATCCC AAGTCTGTGC AGCAGGGAGC CCCATGCCCC
2951 TGGGACATGA ACCCACCTGC GTGGAATGCT GTTTGTGAGG TGTCTACAGG

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FIGURE 1A

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3001 GTTTATAGTA GTCTTGTGGA CACAGAAATG CACAGGGGAC ACTTACGGAC
3051 ACAGAAATGC ACAGGGGAGG CCGAGCATAA CCAGGGGTGA GGGGCAGGCA
3101 GCAGTTGTAG TTACTGCCGC GGGGCACTGC TATGTGCAGG GACAGCCAGC
3151 GCCCAGCCCA TCACCACTCC CTGGGCTGGC TGGCAGGTAT GGCACCCTGG
3201 GAGCCCGGCA TATACCCAGG GCACCCCTAC GGCTGCCGCC AGTCTCATGC
3251 CCAGGTGGGT GCTCTGGGCT GGAGCGAGGG CCAGGTTTTC GGGCAGGCT
3301 TCCCCAGGCA ATCCTGTGAG CTCCCTTCTA GCCTCTGACC CAGTCTGGTC
3351 TGGCTTGCAT GGATGTAGGG CTTGGGGTGG GAAGTTCAGG TCCTGGCTTT
3401 GCCTTTGCCT GATGTGGATG AGCAGCTCAC ATGCTCAGGG CCACCTGAGA
3451 CTGTCACTGC TCTCCCTTGG CTACTGGGAG GAGTCACTGA GAGCTTCGTT
3501 ACCCTTGCTG CCTTGGCCAG GGCACACCCT ATACCTCCTC ATCTGCTCTT
3551 CCCCTCCGTC CGCCCTTCTG GGCAGGTAGC AGTCCCTGGC CTCTCCCCCT
3601 GGCTGATCAC TCTCCCTCAG GCAGTGGAGA TCTGCGTCTG GACACCCTCA
3651 GATCCTGTCA TTGCCTGCCC AGAGTCCTTC AGGGGCACCC CTCTGCCTTG
3701 GTGTGCGGTC CAGGGCTCTC ACCCAGGTGC CGCACCCCTCT GGGGTCTTCT
3751 GTCCAGTCC CTTGCCCAT GTGCTGTAC TGACTCTCCT TGGGACTCGC
3801 CTGCCGTGCTC AGAGCCCTGC AGGGCTTGGT CAGCTGCCTG TTCAGTGTCA
3851 ACACCTCCCT GCACATCTTA AAACCTGGGT TTATTTTCG TGAAGGAAC
3901 GTGTTGGGAC CCTTGACATC TGTCAGGTTT GCACATGCTG TTTTTCCTTC
3951 TCAGCCCACG TGTTCTCCCC CACGTGGGGT AGCAGCAGGA CAGACAGTGA
4001 ATCACAGAGT CTGCCCTGAG CAGAGGCTGC TGTCCCTGGG ACTCCTAGCC
4051 ATGGTCAGAC TGTACAAAAC GGTTTTCCAG AAATGAAATG TAAATCCATT
4101 TTTATACTGA AAATGTTACT GAAAGTCACT TTTATGAGCA TCTGCCTTAA
4151 TAAACAGACA TTGATTCCTT TAAAAAATAA AAAAAAATAA AAAAAAATAA
4201 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA (SEQ ID NO:1)

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**FEATURES:**

5'UTR: 1-33  
Start Codon: 34  
Stop Codon: 2197  
3'UTR: 2200

**Homologous proteins:**

Top 10 BLAST Hits

|  | Score | E     |
|--|-------|-------|
| CRA 18000005000949 /altid=gi 4505027 /def=ref NP_002331.1  lano... | 1530  | 0.0   |
| CRA 18000005227733 /altid=gi 4808278 /def=emb CAB42828.1  (AJ23... | 1524  | 0.0   |
| CRA 18000005013642 /altid=gi 1098635 /def=gb AAA91023.1  (U3135... | 1315  | 0.0   |
| CRA 18000004977416 /altid=gi 1352388 /def=sp P48450 ERG7_RAT LA... | 1305  | 0.0   |
| CRA 18000005002424 /altid=gi 984145 /def=emb CAA61078.1  (X8780... | 1224  | 0.0   |
| CRA 100000004433519 /altid=gi 8886139 /def=gb AAF80384.1 AF1599... | 689   | 0.0   |
| CRA 335001098658178 /altid=gi 11279144 /def=pir T48782 lanoste...  | 611   | e-173 |
| CRA 18000005223063 /altid=gi 4589852 /def=dbj BAA76902.1  (AB02... | 609   | e-173 |
| CRA 18000005171896 /altid=gi 3688598 /def=dbj BAA33460.1  (AB00... | 607   | e-172 |
| CRA 1000682333668 /altid=gi 6045133 /def=dbj BAA85266.1  (AB033... | 605   | e-172 |

BLAST dbEST hits:

|   | Score | E   |
|---|-------|-----|
| gi 10993792 /dataset=dbest /taxon=96... | 1538  | 0.0 |
| gi 10159427 /dataset=dbest /taxon=96... | 1358  | 0.0 |
| gi 9340844 /dataset=dbest /taxon=960... | 1108  | 0.0 |
| gi 11251687 /dataset=dbest /taxon=96... | 1065  | 0.0 |
| gi 11258382 /dataset=dbest /taxon=96... | 995   | 0.0 |
| gi 10322370 /dataset=dbest /taxon=96... | 910   | 0.0 |

FIGURE 1B

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**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

From BLAST dbEST hits:

gi|10993792 teratocarcinoma

gi|10159427 ovary

gi|9340844 uterus

gi|11251687 muscle

gi|11258382 brain

gi|10322370 colon

From tissue screening panels:

hippocampus

FIGURE 1C

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1 MTEGTCLRRR GGPYKTEPAT DLGRWRLNCE RGRQWTYTLQ DERAGREQTG
51 LEAYALGLDT KNYFKDLPKA HTAFEGALNG MTFYVGLQAE DGHWTG DYGG
101 PLFLLPGLLI TCHVARIPLP AGYREEIVRY LRHIEDKSTV FGTALNYVSL
151 RILGVGPDDP DLVRARNILH KKGGAVAIPS WGFVWLAVLN VYSWEGNLTL
201 FPEMWLFDPW APAHPSTLWC HCRQVYLPMS YCYAVRLSAA EDPLVQSLRQ
251 ELYVEDFASI DWLAQRNNVA PDELYTPHSW LLRVVYALLN LYEHHS SAHL
301 RQRAVQKLYE HIVADDRFTK SISIGPISKT INMLVRWYVD GPASTAFQEH
351 VSRIPDYLWM GLDGMKMQGT NGSQIWDTAF AIQALLEAGG HHRPEFSSCL
401 QKAHEFLRLS QVPDNPFDYQ KYYRQMRKGG FFSFTLDCGW IVSDCTAEAL
451 KAVLLQEKC PHVTEHIPRE RLCDAVAVLL NMRNPDGGFA TYETKRGGHL
501 LELLNPSEVF GDIMIDYTYV ECTSAVMQAL KYFHKRFPEH RAAEIRETLT
551 QGLEFCRRQQ RADGSWEGSW GVCFTYGTWF GLEAFACMGQ TYRDGTACAE
601 VSRACDFLLS RQMDAGGWGE DFESCEERRY VQSAQSQIHN TCWAMMGLMA
651 VRHPDIEAQE RGVRCLEKQ LPNGDWPQEN IAGVFNKSCA ISYTSYRNIF
701 PIWALGRFSQ LYPERALAGH P (SEQ ID NO:2)
```

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2

|   |         |      |
|---|---------|------|
| 1 | 371-374 | NGSQ |
| 2 | 686-689 | NKSC |

[2] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 5

|   |         |     |
|---|---------|-----|
| 1 | 149-151 | SLR |
| 2 | 247-249 | SLR |
| 3 | 149-151 | SLR |
| 4 | 247-249 | SLR |
| 5 | 494-496 | TKR |

[3] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 7

|   |         |      |
|---|---------|------|
| 1 | 49-52   | TGLE |
| 2 | 72-75   | TAFE |
| 3 | 238-241 | SAAE |
| 4 | 434-437 | STLD |
| 5 | 518-521 | TYVE |
| 6 | 591-594 | TYRD |
| 7 | 624-627 | SCEE |

FIGURE 2A

[4] PDOC00008 PS00008 MYRISTYL  
N-myristoylation site

Number of matches: 11

|    |         |        |
|----|---------|--------|
| 1  | 76-81   | GALNGM |
| 2  | 107-112 | GLLITC |
| 3  | 142-147 | GTALNY |
| 4  | 173-178 | GGAVAI |
| 5  | 369-374 | GTNGSQ |
| 6  | 487-492 | GGFATY |
| 7  | 552-557 | GLEFCR |
| 8  | 564-569 | GSWEGS |
| 9  | 571-576 | GVCFTY |
| 10 | 577-582 | GTWFGL |
| 11 | 595-600 | GTACAE |

[5] PDOC00825 PS01074 TERPENE\_SYNTHASES  
Terpene synthases signature

563-577 DGSWEGSWGVCFTYG

**Membrane spanning structure and domains:**

| Helix | Begin | End | Score | Certainty |
|-------|-------|-----|-------|-----------|
| 1     | 95    | 115 | 1.321 | Certain   |
| 2     | 173   | 193 | 0.944 | Putative  |
| 3     | 569   | 589 | 1.311 | Certain   |

FIGURE 2B

**BLAST Alignment to Top Hit:**

```
>CRA|18000005000949 /altid=gi|4505027 /def=ref|NP_002331.1|
lanosterol synthase (2,3-oxidosqualene-lanosterol
cyclase); Lanosterol synthase; human lanosterol synthase
[Homo sapiens] /org=Homo sapiens /taxon=9606
/dataset=nraa /length=732
Length = 732

Score = 1530 bits (3917), Expect = 0.0
Identities = 720/732 (98%), Positives = 721/732 (98%), Gaps = 11/732 (1%)

Query: 1 MTEGTCLERRRGPGYKTEPATDLGRWRLNCERGRQWTWYTLQDERAGREQTGLEAYALGLDT 60
MTEGTCLERRRGPGYKTEPATDLGRWRLNCERGRQWTWYTLQDERAGREQTGLEAYALGLDT
Sbjct: 1 MTEGTCLERRRGPGYKTEPATDLGRWRLNCERGRQWTWYTLQDERAGREQTGLEAYALGLDT 60

Query: 61 KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTDYGGPLFLLPGLLITCHVARIPLP 120
KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTDYGGPLFLLPGLLITCHVARIPLP
Sbjct: 61 KNYFKDLPKAHTAFEGALNGMTFYVGLQAEDGHWTDYGGPLFLLPGLLITCHVARIPLP 120

Query: 121 AGYREEIVRYLR-----HIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL 169
AGYREEIVRYLR HIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL
Sbjct: 121 AGYREEIVRYLRVQLPDGGWGLHIHIEDKSTVFGTALNYVSLRILGVGPDDPDLVRARNIL 180

Query: 170 HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPBMWLFPDWAPAHPSLWCHCRQVYLP 229
HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPBMWLFPDWAPAHPSLWCHCRQVYLP
Sbjct: 181 HKKGGAVAIPSWGKFWLAVLNVYSWEGLNTLFPBMWLFPDWAPAHPSLWCHCRQVYLP 240

Query: 230 SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL 289
SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL
Sbjct: 241 SYCYAVRLSAAEDPLVQSLRQELYVEDFASIDWLAQRNNVAPDELYTPHSWLLRVVYALL 300

Query: 290 NLYEHHSASHLRQRAVQKLYEHIVADDRFTKSIISIGPISKTINMLVRWYVDGPASTAFQE 349
NLYEHHSASHLRQRAVQKLYEHIVADDRFTKSIISIGPISKTINMLVRWYVDGPASTAFQE
Sbjct: 301 NLYEHHSASHLRQRAVQKLYEHIVADDRFTKSIISIGPISKTINMLVRWYVDGPASTAFQE 360

Query: 350 HVSRIPTYLWMLDGMKMQGTNGSQIWDTAFAIAQALLEAGGHRPEFSSCLQKAHEFLRL 409
HVSRIPTYLWMLDGMKMQGTNGSQIWDTAFAIAQALLEAGGHRPEFSSCLQKAHEFLRL
Sbjct: 361 HVSRIPTYLWMLDGMKMQGTNGSQIWDTAFAIAQALLEAGGHRPEFSSCLQKAHEFLRL 420

Query: 410 SQVPDNPDPYQKYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLQEKCPHVTEHIPR 469
SQVPDNPDPYQKYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLQEKCPHVTEHIPR
Sbjct: 421 SQVPDNPDPYQKYRQMRKGGFSFSTLDCGWIVSDCTAEALKAVLLLQEKCPHVTEHIPR 480

Query: 470 ERLCDAVAVLLNMRNPDGGFATYETKRGGHLELLNPSEVFGDIMIDYTYVECTSAVMQA 529
ERLCDAVAVLLNMRNPDGGFATYETKRGGHLELLNPSEVFGDIMIDYTYVECTSAVMQA
Sbjct: 481 ERLCDAVAVLLNMRNPDGGFATYETKRGGHLELLNPSEVFGDIMIDYTYVECTSAVMQA 540

Query: 530 LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG 589
LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG
Sbjct: 541 LKYFHKRFPEHRAAEIRETLTQGLEFCRRQQRADGSWEGSWGVCFTYGTWFGLEAFACMG 600

Query: 590 QTYRDGTACAIEVSRACDFLLSRQMDAGGWGEDFESCEERRYVQSAQSQIHNTCWAMMGLM 649
QTYRDGTACAIEVSRACDFLLSRQMDAGGWGEDFESCEERRY+QSAQSQIHNTCWAMMGLM
Sbjct: 601 QTYRDGTACAIEVSRACDFLLSRQMDAGGWGEDFESCEERRYVQSAQSQIHNTCWAMMGLM 660

Query: 650 AVRHPDIEAQERGVRCLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIIWLGRFS 709
AVRHPDIEAQERGVRCLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIIWLGRFS
Sbjct: 661 AVRHPDIEAQERGVRCLEKQLPNGDWPQENIAGVFNKSCAISYTSYRNIFPIIWLGRFS 720

Query: 710 QLYPERALAGHP 721
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**FIGURE 2C**

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QLYPERALAGHP  
 Sbjct: 721 QLYPERALAGHP 732 (SEQ ID NO:4)

**Hammer search results (Pfam):**

| Model   | Description                                  | Score | E-value | N |
|---------|--|-------|---------|---|
| PF00432 | Prenyltransferase and squalene oxidase repea | 83.9  | 1.7e-22 | 3 |

**Parsed for domains:**

| Model   | Domain | seq-f | seq-t  | hmm-f | hmm-t | score | E-value |
|---------|--------|-------|--------|-------|-------|-------|---------|
| PF00432 | 1/3    | 133   | 154 .. | 23    | 45 .] | 6.6   | 3.8     |
| PF00432 | 2/3    | 547   | 589 .. | 1     | 45 [] | 40.1  | 8e-10   |
| PF00432 | 3/3    | 599   | 647 .. | 1     | 45 [] | 39.4  | 1.3e-09 |

FIGURE 2D

```

1 TCATGACTGC CCCTAGAAGC TTAAGTGTGT CAATTCTCAG ACGTAGTTTA
51 CAGCTTTTTC TTTTCTTTCA GACATTAAAA AGAGCGGATT ATTTTACTCA
101 TAAAAAGTCC AGTCCATTAA GATATCAAAA CTCAAACTCT TATCCAGTTG
151 AAACCTCTTC CCTCACCTAG CTTTGCCAGG TTCAGTGTGA GATTCCATCC
201 AGGCTGAAGC CCCTTATCCC TATTCTTCAT GTTCTACAT GGAGGAACTT
251 ACCTGGAGAA AAACCTCCAG CCTCTTTCTG CTTCCAGAGA AGTAGAGTGA
301 CTCATTTGAT TGAATTTAG AGAACAGATA GGGTGGAGTG TGCTCAGGCT
351 CCTCTGGGTA CTCCTTCTGG GGTCTGTGGG TTGACTGGAG GGGTGTCTTC
401 TGGTGGGCAC TCAATTGCAT AGTGCCTGGT GAGGCAGTTT CATGGCCTAG
451 AGGCTGGGGG ATATGTTTGT CTGACTTACG GGTGATTTAG TAGCTTGCCC
501 TCTTGCTTGC AGATTAAAGC CTTGTCTTTC AAGCTAGGTT TTTAATTTGT
551 GGCAAGAGTG ATATTTTGAT ACCCACCCTT CTTATGCTG TGCTTTTTTC
601 ATCCGTTTCT GAACTGGGAT AGGAAGAGGT GATTATCCTT GATTGTCTAA
651 AACCCTCGTA TTCCACTGTG GGAAGGTGCT CTGTGGGTAT TCTTTTGTCC
701 ACTCTCTCTT CCAACTTTCT CCTCCGCTT GCTGTGGCTC ACCGCCCCCT
751 CGAAGTTAGG CTGGGGGTAG GAATTGAGGA GTGGGTGCGG AAATGCTCAC
801 TAGGCTGGGG CAGTTGTAAC TGGATGTCAG GGCTTCTGTG GGCCAGGTGA
851 AGACATGCTG GGGTCTTCTG TGGGTCTTTC ACCTGACTTA GGGACCCTG
901 GCTGCAGCCT CCAGACGTCA GCCATGTTTC CAACAGTCAG ACGCCCCCTG
951 CCCTGTTGCG CCCGGCTGTC CTTTCCAAGT TCGGTCACTC GCTCTGCCTC
1001 CATCTTCTCT TTCCCTCTGC TGCTAAGGCT TTTCACCTTT AATTCTCTCT
1051 GGGGCCACCC CCAACTCCAG CGACCCCGTG AGCAGCTGAG GCTCTACCGC
1101 GCTCGGTCTT GGCCAGCGAC GCAGCCCTTC CCTGGCGGGG CTCCAGGGCT
1151 TCTGGCCCTT GTGGTCCGCC AGGTGTGGGG GCCCACGGCC TCACCGCGCC
1201 TACCCCACTC CCCCAGCGCA AGCTACGCGG CGCTCAGCTT CCCAGGGACG
1251 CCGGCGGCGC CTTGCGCTCC TCCGCTCCGC CCCGCCCTCC CCCTGGTCTC
1301 GCACTGGAGC CGACGGCCCG CGCCACCTC ACCTCAGGGC GGCTTCCCGC
1351 CCCCACCCC GGCCCGCGCG TCCGGGCAAA TCCTGCAGCG CGAGAGCAAT
1401 TCCCTGCCAC CCGACCTTCG CACTCGCTGT CGCTCGCTCG AGCTCGCTC
1451 CCCACGTCCT TCCTTCCGAC CCGCGGCTGG ACCCTCCTCA CAAATTTCTC
1501 AGAGAGGCTC ACCTCAAAGC GCGGCGCAGC AGGCGGGCTC CCCGGGACGC
1551 AAGCCTCTAG AGGGCGCGCG AGAGGCCCCG CCCCCGCCCT TCGGCCCCAC
1601 CCACCAGCCC CGCCCCCACC CGCACCCACC AGGCCCCGCC CCCACCTCCC
1651 CACCACCCAG CCCCAGCCCC ACCTCCCCAC CCACCAGCCC CGCCCCCAT
1701 GCCCCGCCAA TAAGGCCCCA CCGCCTCCC CCGTCCCGTC GCCTTCACCC
1751 ACCATCCCCG CTCCCTCAGG CCCCAGCCCA CGCCGATGG GGACCAAGC
1801 GCTCCACCAC TGTGGTCGCG TGGCACACC CGGGGTCACG CTCGCGGCGC
1851 TCTGATTGGT TCGTGGGCG TCGGCCACC TAAGCTGAG CGCTGCGCA
1901 GGCTGCGGCC TCGGTAGTGC GCGCGGAGG GCGGGAGGG GCGGAGGGG
1951 CGGGAGGGGC GGGGCTGGGC GGCAGGTCCC GGGTGCAGC ATCTGGCAGC
2001 TGGCAGTGGG CGGCGTAGAG CACTGCAGCA GCAATGACGG AGGGCAGTG
2051 AGTCCCTCG CCCCAGGCTC CTGACGAATG CCGGGTGGTC CTAGGTGCTG
2101 AGGAGAGCGC GACTGGGGCA GTGGGCGGCG GGCCGGCGTT GGGGCGGGG
2151 CTGGGTCGCT GATGGCCGCT GGTCTCAGG TGTCTGCGG GCCGAGGGG
2201 CCCCACCAAG ACCGAGCCCG CCACCGACCT CGGCCGCTGG CGACTCAACT
2251 GCGAGAGGGG CCGGCAGACG TGGACCTACC TGCAGGACGA GCGCGCGGC
2301 CGCGAGCAGA CCGGCTGGA AGCCTACGCC CTGGGGCTGG ACACCGTAAG
2351 TTGCTTCCGC GGAGCGTCAG CGAGCTCGG ACCCTGAGGG GTGAGCCGTG
2401 AGGAGCACGT TTTCTCTCAG AAAGCGGGT GGGAGGACCC GGCCAGCGAC
2451 GCCCATCCCC AAGCGAGCG CCCACGGGAA CTGCGTTCGC GGGCCCCCTC
2501 GCTTCAGCCC CTTCTCTCT AAACCACGCA TAGGAGACTC CTAATGTTTT
2551 ATTTTTTAGC ACCTTATTTT GAGATAATTT TTGACTTATA GGAGAGTTGC
2601 AAAGATAGTT GTAACCTTGT TTTTATTCAC AAAAAGTGTT TGGATCCACT
2651 GTCTTAGTTG TGTGCATTGT AAGAGATTTT GGTGCTCAGA GTCTGCAGTG
2701 TAAACAGGGT CTCCTGCCGA GCCCCGCCA CCGAGGGAAA GGCTGTGCCG
2751 CCCCTTGGGC CCTCTTTGAG AGGCCCCAGT CCCAGGCCA GGTGCGCAC
2801 CGTGCCCCAC CTACAGTCT GGTGCTTGG TTTATTCAG ACATCTTGA
2851 GAAGTTTGTG AGAATACATG ACTGGCAAA AAAGCAACGA AAATGTGCAG
2901 CTGTTCTTTT ACTTTGCTGA GGTGTGATGC TCTCATCAA GAGTTTCAGA
2951 CTTTTGATGG AAACAGCTGA AACTTTTAAA GTAATTTACA TTCAGTGT

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FIGURE 3A



```

3001 TGACTTGGGC TGTATGTGAA GAGGGTTCCT CTGGCCGGGC AACAGTCCCG
3051 TCAGCTATCT CTTTTTTTTT TTTTCGATCT CTTTGCAGAA GAATTACTTT
3101 AAGGACTTGC CCAAAGCCCA CACCGCCTTT GAGGGGGCTC TGAACGGGAT
3151 GACATTTTAC GTGGGGCTGC AGGCTGAGGA TGGGCACTGG ACGGGTGATT
3201 ATGGTGGCCC ACTTTTCCTC CTGCCAGGTA GGAGTATGCT GCCCCAGCCT
3251 GATGGTATGG CCACCCCTGA TCACCCCTGG GATCCTGGCC CAGCCTGGTC
3301 TAGGGTTTTG ATGAAGCAGG TGAAAATCCA GGGGCTCACA AGAAAAGGGC
3351 TGGCAAATC TGCCCTATGT CAGAGTCGTC CTGCTATTGG TCTAGGGGAT
3401 CAGCTAGCCT TGCCAGTGTA GGGTGACAGG CTCCTTGATA AGAGAAGCAA
3451 GTGGTTCTCT AGGGCTCTGT GTTGCCCTGA GGGAGGAGGA AGGTGGGCTT
3501 TGAAGTCTCA GTACAGGATG GGATGGACAT TCCAGGTGGA AGGCCAGCC
3551 TATGCCAAGG GCGCTTAGGT GGGCAGAGTG GTGGGTGGGG AGCTGATATC
3601 TGCTGTGAAC TTCCTCGGGG CTATTGCAGG AGAGCTTCAG GTTCAGGCTG
3651 GTGAGTAGGA GGAGCATAGC AGTTGGACTG CCTGGGTATT GAACTGATTT
3701 GGCTACACAA GACTATTTTG CATCCTGGGA GTGTTTCTCT ACAGAAATCC
3751 TCAGCCTTGT AAAATGGGAA ATCCCTCCT ATGAATTTAT GCAATAGGAC
3801 TTTTTTCCCT AGTGACTTGT AATCACATTG TTTCAATGAC GTGAATTCCT
3851 ACATAAATAG GTTTGTTC TGTGATAACT CTTACTGATA CATCATTTTC
3901 TTTTCTACG CTGACTTTGT AATAGATAGA AAGTCCTTAT ATACCTTTGT
3951 TGCCTTTCTT TTTAAACAT CTCTTACCTG TGTCTATTCA TTTACTCATC
4001 CAAATTGCCT TTATCCTGAT TTTGTCCCAG ACTTGAAATG AAGTTGCAAT
4051 AGGCTTATAT GTTAGTTTGG GAAGAGTTGG CCTTTAACGT TAAAAACAGT
4101 TCCATGGTGT TTACTGTAGG CCAAGCCCTG CTCAAGGCCT GTTCTTCTTT
4151 TAGTCCCTAG AATAAGCCTA ATGAGATACA TTAGAAAGCT GAGGCACATT
4201 TATTCAGGT AACCAGACTA GCAGGAGGAG CACTGGGATC CCCATCTCTG
4251 CTTTGACTTC TAGCCCTGCT GCCACCTGGA CTGTACAGCA TTGAGTTTTT
4301 CTGTCCCTGG ATTTGAGGGC CTGTCCCTAG GGGAAAGTCA GGTGCTCTTC
4351 TTCCCTTGGC CCCATCAGGG CCTGTTTAGA CTGTCTCAG GGCTCGTGGT
4401 AAGGCAATGA CATAGAGTTG GTCAGGAGAT GGGTCAGCCC CACTTTGCCT
4451 CTGTAGCCTG ACCTGTGACA GGATTGGAAT CAGGTTTGGT CATGTGCACA
4501 GTGTCAGGCA TGCAGTGGTG CTTGGTCAGT GGGGATTA CTGTTGTTTG
4551 TTCTTGCTGC TTTGGCTCTG GGCTTAGCTG GCTGGGACCC TTCTGTGGG
4601 CTGGCTGTGA GTTGGAGTTT TTTTGTATTT TTTTTTTTTT TTTGAGACAG
4651 CGTTCGCTCT GTTTCCCCAG GCTGGAGTGC AATGGCACAA TTTTGGCTCG
4701 TTGCAGCCTC TGCCCTCTGG GTGCAAGTGA TTCTCTGCC TCAGCTCCT
4751 GTAGGGTCCA GCCCCACAGG GTCGGTAGGT TTTTCTCCCT GTGTGCGGAG
4801 ATGAGAGATT GTAGAAATAA AGACACAAGA CAGAGAGATG AAAGAAAAGA
4851 CAGCTGGGAC CCGGGGACC ACTACCACCA AGACGTGGAA ACCGGTAGTG
4901 GCCCTGAATG CCAGGCTGCG CTGATATTTA TTGGATACAA GACAAAGGGG
4951 CAGGGTAAGG AGTGTGAGCC ATCTCCAATG ATAGGTAAGG TCACATGGGT
5001 CACGTGTCCA CTGGACAGTG GGCCCTTCCC TGCCCTGGCAG CCGAGGCAGA
5051 GAGTGGGAGA GAGAGAGAGA GAGACAGCTT ATGCCATTAT TTCTGCATAT
5101 CAGAGACTTT TAGTACTTTC ACTAATTTTG CTACTGTTAT CTAAAAGGCA
5151 GAGCCAGGTG TACAGGTGG AACATGAAAG TGGACTAGGA GCGTGACCAC
5201 TGAAGCACAG CATCACAGGG AGATGGTTAG GCCTCCGGAT AACTGCGGGT
5251 GGGCCTGACT GATGTCAGGC CGTCCCACAA GAGGTGGAGG AGTAGAGTCT
5301 TCTCTAAACT CCCCCGGGA AAGGGAGATT CCCTTTCCCG GTATGCTAAG
5351 TAGCGGGTGT TTTTCCCTGA CACTGACGCT ACCGCTAGAC CACGGTTGGG
5401 TCCGCTTGGC AACGGGCCTC TTCCCAGATG CTGGCGTTAC CGCTAGACCA
5451 AGGAGCCCTC TAGTGGCCTT GTCCGGGCTT AACAGAAGGC TCTCACTCTT
5501 GTCTTCTGGT CACTTCTCAC TATGTCTCTT CAGCTCCTAT CTCTGTATGG
5551 CCTGGTTTTT CTAAGTTAT GATTGTAGAG CGAGGATTAT TATAATATTG
5601 GAATAAAGAG TAATTGCTAC AAACATAATG TTAATGATAT TCATATATAA
5651 TCATATGTAT GATCTAGATC TAGTATAACT CTTGTTGTTT TATATATTTT
5701 ATTATACTGG AACAGCTCGT GCCCTCGGTC TCTTGCCCTG GCACCAAGGT
5751 GGCTTGCCAC CCACAGCCTC TCGAGTAGCT GGGATTACAG CCATGTGCCA
5801 CCATGCCCTG TGAATTTTGG TATTTTGGT AGAGACAGGT TTTCACCTTG
5851 TTGGTCAGGC GTGCTCGAA CTCTGACCT CGTGATCCCC CACCCCCCAC
5901 CCCAGCCTC CCAAAGTGCT GGGATTACAG GCGTGAGCCA CTGCACCTGG
5951 CTGAGTTGGA GCTTTTCTTC CCTCTTTTGG GACTTTGGAA AATGCTCTTG

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FIGURE 3B

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6001 GTCCATGATG CTATGTAGAC AGCTCCCGTT GACTGTGGCC TGTGCGGCAT
6051 TGGGCAGCAC TCTGGTGAAC ACTGAATCGG GTCTGACCTC CTAGCCCCAC
6101 CATTACTTGG CTGAGCCTCA GTTTCCTTGC CTGTAAATC AGGAAGATGC
6151 TGGCTCTGCT CCTCTCTGCA CATTTCCTCCG TCCTAACAAAC ATTATAACTG
6201 TTAGGAAAGA GACGGGCTTG TTTTGGGATG GCTCATTTTA TGTGACCCTG
6251 TCGCGTGTCT CTGAGTCCAT CTGCCCTTCT TCCAGGGTGT AGGGACCAGC
6301 CCCACAGGGT CGGTGGGTCT CTCCCTGTGT GCGGCGATGA GAGAGTGTAG
6351 AAATAAAGAC ACAAGACAAA GAGATAAAAG ACAGCTGGGC CCGGGGGACC
6401 ACTGCCACCA ATGCATGGAG ACCAGTAGTG GCCCCGAATG TCTGGCTGTG
6451 CTGTTATTTA TTGGATACAA AGCAAAAGGG GCAGGGTAAA GAGTGTGAGT
6501 CATCTCCAGT GATAGGTAAG GTCACATGGG TCACGTGTCC ACTGGGACAG
6551 GGGGCCCTTC CCTGCCCTGGC AGCCGAGGCA GAGAGAGGAG ACACAGAGAA
6601 AGAAACTTAA TGCCATTATT TCTGCATATC AGAGACTTTT AGTACTTTCA
6651 CTAATTGACT ACTGCTATCT AGAAGGCAGA GCCAGGTGTA CAGGATGGAA
6701 CATGAAGCGG GACTAGGAGC GTGACCACTG AAGCACAGCA TCACAGGGAG
6751 ACAGGCCCTCC GGATAACTGC GGGCAGGTCT GACTAATGTG AGGCCCTCCA
6801 CAAGAGGTGG AGGAGCAGAG TCTTCTCTAA ATTCCCCCGG GGAAAGGGAG
6851 CCTCCCTTTC CCGGTCTGCT AAGTAGCGGG TGTGTGTCTT TGACACTTTT
6901 CGCTACCGCT AGACCACCGT CCGCTCGGCA ACGGGCGTCT TCCCAGACGC
6951 TGGCGTTACC ACTAGACCAA GGAGCCCTTT TGCTGGCCCC GTCCGGGCAT
7001 AACAGAAGGC TCGCACTCCT GTCTTCTGGT CACACCTCAC TATGTCCCCT
7051 CAGCTCCTAT CTCTGTATGG CCTGGTTTT CCTAGGTAT GATTGTAGAG
7101 CGAGGATTAT TATAATATTG GGATAAAGAG TAATTACTAC AAATAATGA
7151 TTAATGATAT TCATATATCT CTAAGATCTA TATCTGGTAT AACTATTCCT
7201 GTTTTATATT TTATTATACT GGAACAGCTC GTGTCTCGG TCTCTGCCT
7251 TGGCGCCTGG GTGGCTTGCC GCCCACACAG GGCATGTCTG GATGGTTGA
7301 ACACTAGGGC TTCTGATGCT CTAAGCCAGA GTCAGGTATT CATTCCATGG
7351 CACATGTGGC TGGGGTCTGC CCTGAGACCT GTCCCGTGCC AGGCTCTGGG
7401 GGCACATGGC TGATGGAACC AAGCATGGGG AGTGAAGGTG GAGGGTGGCC
7451 TGTGAGCACC ATGCCGTAGA GGACCAGGCT GGGGACGGAA GGTCTTAGT
7501 GGATAATATT TATTGTCTCT GCCTCCCCC TGACATTGTC AAAGCGGCAT
7551 ATGCTTGTAA AAAATTTTGA AAACAGAAAA ATATAAATAA ATAAGTAGGT
7601 ATTACCACAT GCAAGGGTGA CCAATTTTGT ATTTTCTTTC CCAGCAGATG
7651 TTAAAGCAAG ACCAACAGTC TCCCCTCATG GAAGGCCAC TGATCTAAAA
7701 TGCTGGTTCC TTTTGGACCT TCAGGGCACT TGGGGGAGAC CTTCTGAGG
7751 TGCTGTGAGC TGCTGTGGTGT TTCTCAGACC CAGGTGGTCA TGGGAGCCAG
7801 GCGTGGCTGA GTGGCTCTA CAGGCCCTAG GCAGGGAGCA TCGCCTGTGC
7851 TGTGGCTGAC GTTCTTCTG GCCCTGTTC CAAAGTTCCC CATGGGGGCC
7901 TGGGAGGAAT GGCTTTTCCA GGGGGTGTTC TTATGAGAAG GAGGTAGCTC
7951 CCTGTTGGAG TGAGGTGCTC AGGAGGAAAG GGGCCTGGTC TTAGCAGTCA
8001 TGACCACCTG TCCCCAGTGA GGAACATCTC TCCTGCCACA CAGGCCTCCT
8051 GATCACTTGC CACGTGGCAC GCATCCCTCT GCCAGCCGGA TACAGAGAAG
8101 AGATTGTGCG GTACCTGCGG TCAGTGCAGC TCCCTGACGG TGGCTGGGGC
8151 CTGTGAGTGT GCCTGCCCTT GTGTCACTGC ACATGTGCAT GTGTGTGTTT
8201 TCATGATGTA GGAGATGCTT GGGTTTCCAG GCAGCTGCCA GGGGTTAGGA
8251 GTGATTGCAG CTGTGGGTGT GGGGTGGGTG AGGGAGAGAC TAGCAGGCGG
8301 GGAGTGGGCT GAAGGCCATG CAGGTGGGGC CTCGGCTTCA CATCTTTTGT
8351 TAAATGGATT TTGTGGCTGT TACGACACTC TTGAGACCCA CATGTGAAAA
8401 CTGTCAGTCT GTTATCACTT AAGACAGAAG AAAATTGCCC TTGACTCTGG
8451 GCTGGCAGCA GGTGGAGACA AGGCCTGACA GCTTTCCTG CATGTGGCAC
8501 ACACTTTGGG AGCAGAGCCA TAGCCCAAAG TGGACCGCCC TTGAGCTAGA
8551 AGTGTGACT CAGGCGTGGG AAGGTGTAGA GCAGGCGGGT CACGGTGAGG
8601 AAGGAGTGGG GGGCTCAGTT GTCATGGGAG GTGCATGAAT TCGTACTGCA
8651 GAGTGGCTGC TCAGGGGTCT CCTGTGTTGA CATGTTATGT CAGGTTAAGC
8701 CATTTTAGCA TTCTTAGTTT TCTGAGGAAA CTCCACAGAA AGTTTTGCTT
8751 TATTTCTTAG AAGTAAGGAC AGATACCGGT TTCTCACCTG TCCTCTGCTC
8801 CTGTAGGCAC ATTGAGGATA AGTCCACCGT GTTTGGGACT GCGCTCAACT
8851 ATGTGTCTCT CAGAATTCTG GGTGTTGGGC CTGACGATCC TGACCTGTA
8901 CGAGCCCGGA ACATTCTTCA CAAGAAAGGT ACGGCATGTG CAGCATGTGC
8951 TGGGCCAGGG GTTCGTGTCA ACTCGATAAT GAGCTCTCAC AAACGAGATA

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FIGURE 3C

9001 CAGAAAGATG CACTTGCAGC TGAACAGTG GGCAAAAGCA CATGAGCAGG  
9051 GAATTTGTCA AAGCAGAAGT AGGCAGACAC TGT'TTAACCT AGGCATCATT  
9101 TTTTAAAAA GCAAATTAAG AGCCAGGCAC AGTGAGTGGC TCACGCCTGC  
9151 AATTCCAGCA CTTTGGGAGA CTGAGGTAGA AGGACCACTT CAACCTAAGA  
9201 GTTCGAGGCC AGCCTGGGCA ACATAGTGAG ACCTGGTCTC TACAAAAACA  
9251 ATAAAAATATT AGCCAGGTGT GATGATATGC ACCTGTAGTC TCAGCTACTT  
9301 GGAGGCTAGT AAGGCAGGAG GATCACTTGA GCCCAGGAGT TCTGGGTTGC  
9351 AATGAGCTGG TTGTACTACT GCACTCTAGC CTGGGTGACA GAGTGCAGCC  
9401 CTGTCTCTAA TAAAAATAAA AAGCCAAGCA AACTAAGACA ACCAGGTAAT  
9451 TCTGTTTGT TCTGAATTG GCAAAACTT AAACGAACCG TGT'TAATATG  
9501 TCCACCTTCT GGGGGGCAGC CTGGCTGCAG GCAAGAGCAG CCCTGGAGCT  
9551 GTTACCTTCC AAGCTGATCG TCTACCTCTC CAAGCCCGGG GCTGTCCACC  
9601 TCTCCAAGCC CGGGGCTGTC CACCTCTCCA AGCCCGGGGC TGTCCACCTC  
9651 TCCAAGCCCC GGGCTGTCCA CCTCTCCAAG CCCCAGGTTG TCTTACCTCT  
9701 CCAAGCCCCA ACTGTCTACT TCTCCAAGCC CTGGTCTGGC TACCTCTCCA  
9751 AGCCCTGGGC TGTCCACCTC TCCAAGCGCC AACTATCTTT CTCTCCAAGC  
9801 CCTGGCCTGG CTACCTCTCC AAGCCCCAGG CTGTCCACCT CTCCAAGCCC  
9851 CAACTGTCTA CCTCTCCAAG CCCCAGCCTG GCTACCTCTC CAAGCCCCTG  
9901 GCTACCTCTC CATGCCCGGC CTGGCTACCT CTCTCTTTGC CTATAGGCCC  
9951 TGAGGGGCAA TTCCAGCCCA AGGGAATCCA TGGCTCCTGC TGTCCAAGA  
10001 AAACCTAGTT TATGTTGTGG CTCTGCAGAG CCTGGCCTGG TCTTGTCTCTC  
10051 TGTGTTTAC AGACCTTCCG TAGCCAGTCC CACCTGCCCT GCTCTCTGCT  
10101 GCATGCGCAG GGGCCTCCTG TCAGCTCCTC AGAGACCCCT ATTATCCCAG  
10151 GGCTCGCCAT GCACTGCCTC CTTCGCCTGG AGCCTCTTAC CTTCCACTCC  
10201 TGCCCCGCTG GCTCACACTT TACGTGTTC TTCTTTGAGG ACCTCTTCCT  
10251 GACCTACCGT GCCAGGTGGA GTGTCTGTT ACGCATTTCTC ATGAGATCCT  
10301 GCCTTCTTTC TTGGTGAGCT TGTCATAATT GTCCTCAGTT CACTGTGAGC  
10351 CTTTGGTGTC GTTGATGCTG CGTCCCAAG GCTGCTGTCC GGT'TCCACC  
10401 ACACCTCTGG CGCCTGCCTG GTGAAGGAAC GTGTTTAGGC TGCAC'TTGC  
10451 CTAGTAGCTT TGTGGGTCTT TATTGACTTT TGCATACCTT TTGGGGTTTG  
10501 GAGCAGGGAC TCCTCAGAAG CATGTTTAGA TGGTGTGGCT GTGCCAGGAC  
10551 TGCTGCTGCT GAAGTGGCTC TGGCATGGGG CCAGCGTGCT GGAGCTACTC  
10601 TGGAGTCTAG GGTCGTCTTT GTTCCCATAC AGGACCAGTC TGCCAAGTGG  
10651 AGATGACACA GACTGGGGCA GCTCAGGCTT GGCTCAGAGG GCGAGGCTGA  
10701 GTGTGCGCTG TCAC'TTCCCC ACCTTGCCCT CTCCAGGCGC ATGTGCACCT  
10751 GGGCCCCTCG CTCACCTGAG CACTGAGGTG TCCCTGGACC TTCCCAAGTA  
10801 GCTGTCTTCA TGTGCTCCTT CCTGGGGCCA GGGGTTGCAA ACACCTCTCC  
10851 TGGGGCTGGA CACACACACT CCCAGGAAAG CCACTGGTTC CACCTAGGGG  
10901 GCCGTGTATC CAGGCAAGTT CTCAGCACTC TGGAACTTGC TTTCGCACATG  
10951 GGGGTCGCAA GATCCACATG AGGCTGCCCT TGCCTCATGG AGAGGGGCAC  
11001 ACGTGA'TCC CAGAGGGTGA AGCT'TCCCAG CTAGAGGCAG TGCAGACTTT  
11051 GCTGACAGGA AGCAGATGAC GTGGGCCTAT TCTCTCCCCG CTCAGGTGGT  
11101 GCTGTGGCCA TCCCCCTCTG GGGGAAGTTC TGGCTGGCTG TCCTGAATGT  
11151 TTACAGCTGG GAAGGCCTCA ATACCTGTT CCCAGAGATG TGGTATGTCT  
11201 GCTGTTGATT GGGTTGTTGG GTCGCTGCTG CTGTCCCGGG GAGTAGAGTG  
11251 ACAGGGACCG TGGGTCAAGT GCAGGCTGTG ACAGCAGAGA GGGGTGGGCA  
11301 TTCTGTGGGT GGGTGGAGTT AGGCTCCTGG CAGAGGCCCT GATCAAGCTT  
11351 GAGTCCTGTA GGGGTACAGA AAGGGGAGG TTCCAATTG AGCAGGAAGA  
11401 AGGCTGTGCC ATGGATGGAG GTACCCCGAG TCAGGCTGCA GGCAGGCTG  
11451 GGTGGCTTCC CTCTTGCTGT GGAAGACTCA GCATCTGTAG AAGTGGGGGG  
11501 GTGCCCCCTC CCCAGCCTGC ACAGGGGCGT CCTGTGTTGC TGCTGCTGCG  
11551 TTTGTCTCCT TTGCTGTGTA ATGTGAAGTG TGTCCCGACG TGACACCTCA  
11601 CCTGTGGACT CAGCGTGTGT GCCTTTAAAA GATCAGTGTC TGTGGCCAGG  
11651 TGGGGTGGCT CATGCCGTGA ATCCCAGCAC TTCGGGAGGC CGAGGCGGGC  
11701 AGATCACGAG GTCAAGGGAT CGAGACCATC CTGGCCAACA TAGTGAATC  
11751 CCGTCTCTAC TAAAAATACA AAAATTAGCT GGGCGTGGCG GCGCGTGCC  
11801 CTAGTTTCCA GCTACTCGGG AGGCTGAGG AGGAGAATCA CTTGACCCTG  
11851 GGAGGCAGAG GTTACCCTGA GCCGAGATCG TGCCACCATA TTCCAGCCTG  
11901 GCGACGGAGT GAGACTCTGT CTCAAAAAA AAAAAAATAA GATCAGTGTT  
11951 TGT'TTTTTTA AACAGAACCA CATACTGTTT AAATACCCAG CAAAATCAAC

FIGURE 3D

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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12001 ATTAATTCTCT TATTATCTGG TGTGTGTTTT TTTTGTTTTG TTTTGAGACG
12051 GAGTCTAGCT TTGTCACTCA GGCTGGAGTG CAGTGGCGTG ATTTGGGGTC
12101 ACTGCAACCT CCGCCTCCCG GATTCAAGCA ATTCTCCTGC CTCTGCCTCC
12151 CGAGTAGCTG GGATTACAGT CTCAGGCCAT CACGCCCAGC TAATTGTTGT
12201 ATTTTTAGTA GAGACAGGGT TTCACTATGT TGGCCAGGAT GGTCCTAAAC
12251 TCCTGACCTC AGGTGATCCG CCTGCCTTGG CCTCCCAAAA GTGCTGGGAG
12301 CCATGAGCCA CTGCTCCCGG CTTTATGTGG TGTCTTTAAC CAGTGTCTTG
12351 TAACATTTTA TGGCTATCTA TTGAAAGCAG TGGACATCTC CCCAGAAAAC
12401 ACTCGTGCAT ATGAGTTTAC CCCGTTATGC ATTTTGGGAA GTGAGACCCT
12451 GGAACCACAC AGAGCCCTCG CTGGCTTCCT TGAGTGTGTG GGAACCCTG
12501 GTGGGGGTGT CCCCTACAGA GCTATCATCA GGGCTGGGGG GGTCCCTTGT
12551 GTTAGTGCAG TTTTGGTCCG GGGTGGGGGG TGGGGGGTCA AGTTAGGGGA
12601 GGCAGGAAGT GAAGGGGCCG CTCAAGAAAG GACAGCAGCA GTGCTCTGAT
12651 GCAAAGGCCG GGGGCTTAAC CCCGGAAGCC AGTTTGGGTG GTGACGGGGA
12701 GGCACAGGGA TGGTGAGATC ACCCCGGGAG GGTAGACAGA GATACCAGAG
12751 TAGGGGGCAG GGTTAGGGTG CCGCTACCTG AGGCGGGCCG TAGAGCACAT
12801 AGGTGGGGAG GTGTCTTGGG GCCATTCAAA TGCCCGCTGG ACTCTGCGCC
12851 TCGCCCTGTG GTAATGAGCG GCAGAGGAAG GACTGAGACG GCAGTCAGCA
12901 CAGCTGCCAG GGCAGAGGGG GTGTGGGTTC CACACGCTGG TGCTGGTGAG
12951 GGCGTCTCAT CTGCCCCACT TGGGGGGGCC GTCGGTCAGT GCTGCCGCAT
13001 GGGCACGCCA GGGTGTGCTG TGTCTTTGCT GGAGTTGCTT GGAGGGTGGG
13051 TTGGGAGGTG AAAGGAGGAC CACAGACCTG AACCCTCCA GCTGCGAAAT
13101 GCTGGAAGTG TAACCAAAAA TGTGAGAAAA AAAACACCC TTTTAAGTAA
13151 GTGGGTGTGA AAGTGGGCCA AGGCCTGATG CCACAGTCAG GGAGCAGGGA
13201 AGGCTCAGCA TTGCTACCCC TCACTTAAGG ATGGGGCTAG CATCACATAA
13251 GGCATCACAT AAGGATGGGG GCTAGCAGGG AAAGGGAGAG AAAACACATG
13301 AGGCACACAC AGACCTTGGG AAGCTGGTGG AGCTGTGCTA ACGTCAGCAG
13351 ACCAGTGATC AAAGACCCAG GCCTTGGGGA GATTCCACAG ACCTACAGAC
13401 CTACAGTTTC TTTTCTCTTT CTTTCTCTTT TTTTCTTTT TTTTGAGACA
13451 GAGTCTCTCG CTCTGTCAAC AGGCTGTGTG CAGTGGCACA ATCTCGGCTC
13501 ACTGCAACCT CCTCCCAGGT TCAAGCGATT CTCTGCCTC AGCCTCCCAG
13551 GTAGCTGGGA TTGAGGCAC ACACCACCAT GCCTGGCTTA TTTTGTATT
13601 TTTAGTAGAG ATGGGGTTTC GCCATGTTGG TCAGGCTGGT CTCAAACCTC
13651 TGACCTCAAG TGATCCACCA GCCTCGGCCT CCCAAAGTGC TAGGGTTACA
13701 GGCGTAGGCC ACCGTGCCCC TCCTAAAGTT TCTTAAATAC ACTTTTAAAA
13751 GTAAACTTTA AATTTTGGAG TAGTTTCCAA TTTCTGAAAA AGTTGCAAAAG
13801 ATAGCCAAGA GTGTCCCTG GGGCCCTCAC ACCATATCCC CATTTGTTGAT
13851 GTTTTAGTGT ACCAAGGTAC GTTTGTGTGA GCTAAGAAAC CCACGGACAA
13901 TCCTAAGCAT TTAGGAGCTC CATCACCTGG TTTTAGGATG CAAAATGCTG
13951 ACCGAAC TAGGTGCAGC TCCTCAGAGG GTGCACCTAT GGTTCAACTG
14001 TGCCCTCAG GAGCACGGTT GGGAAATGCC CGCAGATGCA CTGACGTGGT
14051 GGGGAATAGC CATCCACCAG TGTTCTGTGCT TGAAAGGGCC CAAGGTATGG
14101 ATGCTGGCGG AGGGGGCAGG CTTGAGTCTT GGGGTCTCCC ACTGACTCCT
14151 GCTGTTGCCC CAGGCTGTTT CTTGACTGGG CACCGGCACA CCCCTCCACA
14201 CTCTGTGCCC ACTGCCGGCA GGTGTACCTG CCCATGAGCT ACTGCTACGC
14251 CGTTCGGCTG AGTGCCCGG AAGACCCGCT GGTCCAGAGC CTCCGCCAGG
14301 TAGGACCTCA TCAGGGAACA AAGTGAAGGC CTCTGGGGCT GGGACCCACA
14351 GGGCCTGGGG CTTCTGGAAT CTAACCACAC CTGTCCACTC ACCTGGTGGC
14401 CCTGTGGAGC GGAGAGCCCT GTGGAGCAGA GCCTCCACCT TCCTCCATCC
14451 TATAATAAAC AGTGAGCAAG CTCTGCCCAG AGGGGACTTG TGCTATGGGA
14501 CAGTCAGTAG CTGTAGCCCA GGGTTCCTGG GGGGACTTC CAGGACTCAA
14551 GGGATGCAGG AGGCAGATGT GCACTGTGTC CTCTGGAAGC AGGCCTGAGG
14601 CGAGGTTTGA GGTGCAGGAT GTTTATCAGG CCTGCCATGG GGAAGAAGGA
14651 GGGGCAGAGG GAGGAAATGA GCTTCTGGGC AGACCTGGGA CTCATGGAGC
14701 TGGGGAGCTC CTCAGAGCGG TCCTCCATA GGGGGCCTTC ATGTGCCCTC
14751 GGGGTCAGTT GCTGGAGGGA CCCCCACCA GGAAGGGACT GGCCAGGGC
14801 CCTGAGGGCG CATGGTGGGA GGCCACCCCT CTTGGTTTGA GCCAGGCTTA
14851 CCAGGTGCTC CCAGGCCCA AGGCTCAGAC ACTGCCCTTA CCAGGAGCTC
14901 TATGTGGAGG ACTTCGCCAG CATTGACTGG CTGGCGCAGA GGAACAACGT
14951 GGCCCCGAC GAGCTGTACA CGCCGCACAG CTGGCTGCTC CGCGTGGTAT

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FIGURE 3E

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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15001 ATGGTGAGCG CCTCCTGAGG GGCCGGCAGG GCAGCCCAGG GTCAGGGTCA
15051 GGGTGTGCGC CACTCATTTCA CGCACTCATC CCCTGCCAGC GGCACTGGGC
15101 CACCTCCTCT GTGCCAGGCC CCAGGGGGCG GGATCTCATC GCCCTGCCCC
15151 TCCACCCTGA GAACCAGCTG GTCTTCTACT CTCAGGAGTC CACCCTGTGC
15201 AAGGGTGTGT GGTAGGAGGT GTGGGGCAGC CCCTCCTGGG CAGGGAAGGA
15251 GGAGCTCAGA GACCAGGCCT GGGGGTGGGT GGGAGGGGGA AACCTGGGG
15301 AAGGGCAAGT CCAGGCGTTG CAGTGCATGG AGCTCCAGGC TGAGGCCAGT
15351 GTCATGGTGT CTGGCATCCA CTGACCCCTG TCCCCTGTAG CGCTCCTCAA
15401 CCTGTATGAG CACCACCACA GTGCCACCT GCGGCAGCGG GCCGTGCAGA
15451 AGCTGTATGA ACACATTGTG GCCGACGACC GATTACCAA GAGCATCAGC
15501 ATCGGCCCCG TCACTGCCCC TGCCCGGCCT CTGACTGCAG CCCCTGGGG
15551 TTGAGTCCG AAAGTGAAGT CCTAGAGGCC GGGCTGTGAG CTGGGAGTGG
15601 GGTTTCTCTG AGCCTGGTGT ACCTCCATTT GGGAGGTGGC CCTCTGATCG
15651 CACAAGTGTC TGAGGGCTTC TGTCTGGAC CCCTGCACGC CCAGCTCAGT
15701 GAAGTTGCC CACCACACTC GACCCCCCGC TTCCGTCCCC CACCGGCTCT
15751 TGTCTCAGT GTGCCCTGGAC ACTCTCCTAG AGCCCCCTCC CTGAGATCTT
15801 GCTGGCTAGC TGGCTAGCTG GGAGGGGTGC TTTTTCCTCA CTGGTTCCC
15851 TCTCCCCAAA CAGTTTATCA TTCGCCATTC TCCCGTGGGG TTAGACATG
15901 CCCAGGTGG GTGGGAGTAG CAGGTGCCAC TCCTGATTCC TCTGCCTAG
15951 CTAGGGACTT GGAGCTCTCA CCTCTGTGGG GCCTGCAGGG GTCCAGGTGT
16001 GGCCAGTTCA GTGACCTTAG AGGGTGCAAT CCCC GGCTG TGCTGGTGCG
16051 TGGCCGCTC CTGACAGAGT CAGCAGGCC TGGGCTGTGC TGCAGCTGCT
16101 GCCGTAGCTG TGCGCGTAGC TGCTGCGGTG TAGTGGGTG GCTTAGGCAT
16151 TCTCTGGACA TACCAGGTG GCACTGGGCC ACTGAGTCCC ACCCTGACAC
16201 TGCATCTCGG ATTTTCTGGG CCTCATGCCA CCTCAGTGA TCACAAATCC
16251 TGACTGACCC TGCAGCGGGT CCCTTGTTTT TTGCTCAGCA GTGATGTGGT
16301 TCTTTGTGGG TTTTGGTTTA ATCCCATAA GAGCACATCT GTACTAAACG
16351 CATTAGAAAC ATGCTTGCAA TTGGATCTTG ACTTGTGAGA TGCATAAGTA
16401 AAAAGTTGGG GGCTCTGGA ACATCTGTG CTGAGGAAGA AGGGGGGCAA
16451 GTGGTCCCTA CTGTACAGT CCTGTCTTCG CATCTCTTCC TGGGCCCTC
16501 AGGCCCTGT CTCTGTCCCT TGTGTGTCT CTAAGGCACC TGGTAGCCCA
16551 TGCCCTCTG ATTTTCTCTG GAACCCCTCG CTTCTCCCTG GTGGAGTGCT
16601 GCTCCTTCTC ACAGCCTAAG GCAGGCTGTG GCCTTGCCG AACTGCCTC
16651 TGTCTAGATT GGGTCTGGG GACACAGTTG TTGCCATCC TCGCTCAGGA
16701 AATGCCGTG AGAGCAGAAG GCCCTGTCC TGGCCCTGAG TGATCTGCAC
16751 GGCACCTTAT GCCTGGGGG TGCTGTGGAT CTGGACGAGA CCTTGTCCCT
16801 GGAGGCTGCT TTGGGTCTGG AGCGGAGCCT TGACAGGGCT GTCTCTCTG
16851 CAGATCTCGA AAACATCAA CATGCTGTG CGTGGTATG TGGACGGGCC
16901 CGCCTCCACT GCCTTCCAGG AGCATGTCTC CAGAATCCCG GACTATCTCT
16951 GGTGAGTGTG GCTGGGATAT GCTGGCGGG CCTCTCACGA AGACTGGATC
17001 TGAGCCCAG CTGCATCCCA GTGAGGGGG CCCCACGGTG CCATCTGGGA
17051 ATACTGCCAG GGAATACCTC CAGGAACCAG CAGTGTGAGG GCTTGTGGAA
17101 GCCACTGAGG GTTGTCTTTG AATTGGAAGA TTTGCCACCC AGTGAAGTG
17151 TGGGGTGTTC CCAGAAGGTA GAGTGAGGAA GGGGGTGGTA GGTAGCAGG
17201 CAGGTTTCTG TTGGCATCAG GAGGCTGTG GACAAGGGGA GCTTGTGAGC
17251 CATGGACTGT GCCCTGGAGG TGGGGCCCT GTCATGGAGG GCAGAGAGCC
17301 GTCCCATGGT GGAAGCTTC CGCTGTACAG GCCTCTTCTC CTGGTGCCCTC
17351 AGCACTGCAC GAGGGCGGCA GGGCTGGCAC AGCTGGGGT CGGGGAGCCT
17401 CCCGTGCCCC CTGCTTGG GTGTGGCCCT TCTGGGTGAG TGTGCTCTGT
17451 TTTCCATAGA GTGTGGCCCT CACCCAGG AGCCAGCAG CCCAGCTGGG
17501 GTGGCATCCA GGCCAGTGCC AGGCTCGGG AGGGACAGA CGGCTCTCT
17551 GGGACCTTCC TGAGTGCAGG GTCTGGGTAG CAGCTGGGCT TCCAGCTTTC
17601 TCCTTGACCC TGACTTGGGC TTTTCTCTCC TCACAGGATG GGCCTTGACG
17651 GCATGAAAAT GCAGTAAGG GCTGCGGGAC TGCGGCTGCA TGCTTCCTTT
17701 GCAATCATGT CTCCCCTTTA TTATTTTCTC TTTGGGGTTC AGAAATAACT
17751 CCTCCTGGAC CAGGTCCCGG CAGCGTGCGA CTAGAGGCTG AGTCAGTTGA
17801 GGCTCTGGC CGTGTCCCTG TGGGTGCTGT TGGTCTCTGT GTGGGTGCCC
17851 ACCGTTCTCG ATGTCTGTCT GCAGCTGTCC TGTTTGCTTT TTGCCCTGAT
17901 GATCTGAGTG GGCTCAGCTG TGTAACGACA GACCCAGAGC TGCAGAAGCT
17951 CTCATCTGT TACTGTGGCA GGAGGTGGCT CTGGTGTAGT GGGGCTTCTC

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FIGURE 3F

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18001 CTCCATGCAC TCTTAATTTA AGGGGCTTCT TCTTAAAGGT CCTGGGTGGA
18051 CAGGACAGGA GCCTGGAGGA CCGTGGTGGC GTGTGGCCGG GCCTGGGAGC
18101 TCCCCGTGGA CTTGGCCTGA GTGGGCTGGA ACCCAGTCAT GAGGGGCACC
18151 AAGCACAAGG AGAGGGGAGG CCGGGTGGAT CCTGGCTGAC CCTGGTCCCTG
18201 TCCTGGCTCT GGGGGCCCTG TAGACCGCAG TCCTGTCCGA CTGGGCTGAG
18251 CCTGCGCCCC TCTGTGCGTG TCAGAAAGCCC AGACAGTGTT GCCCTGTGTC
18301 TTGTGGTCTA AGGAGGGTTA CGCCCTGCGG TGCCTGTCTT CTGTCCCCCA
18351 CCTGATTGAG TGTGGAATG TGGAGTCTCC AGAGGTGTCC TGGGTGTCAC
18401 ATTTGGGATG GATACACGTG GGCCCAACAC TGCCCGCCCC AGGGCTACCC
18451 TTGGTGCCAG GTGCCCCCAG CCACGAGCTT TTACCCAGCT GGCCCTGAGC
18501 TCCCCAGAGG CTCCCCGAGC ACTGTCCGTG TTTTGTGAAA AGGTTTTCAG
18551 AACACATGTA AAGTGGAGGT GAGTAGCAAG CCTAGAGCA GGCCCTGGCC
18601 TCCCTGCCCC TCCCTGTCCC CTCCCTGCCC CTCCCTGCCC AGCGCTCCCT
18651 CAGCACCAGC TCATCAGTGC ACCTCAAGCT GATGAGGGCG TCTGTGTTTT
18701 GACAAAATTG CTCTGAGGTT GTCACACCA ACAAACTTAT GACGGTTCCT
18751 GAGTGTAGTC CTCACGTTGT GGCTGGTGTT TGTGAATCAG GATTGAGGCC
18801 AGGCCCTGAC AGGCCCTCAG TTGTTGGTCT TTGAGCTCCT GTTAGTCCAG
18851 CCGTCTCTCG TGGTCTCTTT TCTCCTCCTG GAAGGTTTGT TCCTGAAGGG
18901 CTTACATTTG CAGATCTGAC TGGTTGCTTC TTATGTTCCC TGAGTTTTTG
18951 TAAACTGGCC AGGCCCTGAG GCTCGATCCC ATTGTGTTTC TTTGGCGAGA
19001 ATGCTTTTCT GGTGGTCCCT GCCTTGTCCC TCCAGTGCAC GATGTCTGGA
19051 TGCCCTTGCC ACACACCACC CCCTGCCCAG TCCCCATGTC TGCTGGTCA
19101 GTGCCCAGCT CTGTCTCACT AGGGTTTGGT CACCGGCCCT TTGAACTGAG
19151 ACCAGGCTGT GTACCTGTGA GCCCAGCTCG GGGTGAGATT TGAGGTGGAG
19201 CCTTCCAGC CCTGTGCAGA ATTCCCATCA CCTCCAGGTG TACTCAGAAA
19251 TGGGGATCAT TGGCCAGGTG CGGTGGCTCA CGCCTGTAAT CCCTACACTT
19301 TGGGAGGCCA AGGTGGGCGG ATCACAAGGT CAGGAGATAG AGACCATCCT
19351 GGCTAACACG GTGAAACCCC GATGCTACTA AAAAATACAA AAAAAATTAG
19401 CTGGATGTGC TGGCAGGAGC CTGTAATCCC AGCTACTCCG GAGGCTGAGG
19451 CAGGAGAATG GCGTGAACCC AGGAGGCGGA GCTTGCAGCG AGCTGAGATC
19501 ACGCCACTGC ACTCCAGCCT GGGCAACAGA GCGAGACTTC ATCTCAAAAA
19551 AAAAAAGAAAT GGGGTCAATT CCAGGCATCA CCATGACTGA GGTGCGCCAC
19601 TGTCATTGGG TGAGAGCAGC TGGATGCTCT ATGTGTAGGT GCTGGAGCCT
19651 CTGAGGGATC GTCCAGTCCCT AGAAGTGTCC TCAGAGGGAC ACTGTCCTGC
19701 CTGGTGGCCC ATGAAGAAAG GGAGGGCTCC CTGAGTCTCC CTGACGTGTG
19751 TCTGCCTGCA GGGCTCAGCC TTCTCTGAGG CCCTTGTCAG CCATGAGGGG
19801 TGCCAGGGC TCAGAGCCTG AGGCTGAGCG TTGGCTGGGT GGGAGCCCCC
19851 ACACCTGGCC CTGAGGCGCC CATTTGATCC TGGAGGCGAT GGCTGGGAGT
19901 GGGAGGGGCT GCATCTGCTG CTGTAACACC ATCCTTTGTG TGTAGGGCAC
19951 CAACGGCTCA CAGATCTGGG ACACCGCATT CGCCATCCAG GCTCTGCTTG
20001 AGGTTCGTGG CTCTTCTCT TTTCTCAGCC TCAGCTGACC TTCTGTGCA
20051 CGTAAGCCCA CGCATCCACC TGAGGGCAGC ACTGCTGGCC ACACACTTGC
20101 CACTCCTCGA TACTTCCAGT GACCTGGGCT CTGGCCTCTG GCTTCAGAGG
20151 GTCGTGCTGT GGAGGGGGCG GCCTTGGCCA GCAGCCTTGG GTGTTGGGCT
20201 GGGTCGGGGG CCTTGGGAGG GCAGGGGCTG GAGGCTGTGT GAGAAGGGGA
20251 GTCTGGTGAA GGCTGTTTCT GAGAGTGCAG GCAGGAGTGG GACTCCAGGC
20301 TCTTCTTAGA ACTGGAAC TGTTGGGCCAG GCACGCTGGC TCACACCTGT
20351 AATCCAGCA CTTTGGGAGG CCGAGGAGGG TGGATCACGA GGTCAGGAGT
20401 TCAAGACCAG CCTGGCCAAG ATGGTGAAAC CCCGTCCTA CTAAAAGTAC
20451 ACAAAAATTA GCCAAGCGTG GTGGCGGGCA CCTGTAATCC CAGCTACTTG
20501 GGAGGCTGAG GCAGAGAATT GCTTGAACCC GGAAGTGGA GGGTGCAGCG
20551 AGCCGAGATT GTGCCACTGC ACTCCAGCCT GGGTGACAGA GAGAGGCTCC
20601 GTCTCAAAAA AAAAAAAGAAC TGGAACGTGT TGTATATGGGC
20651 ATTCTCGAGC CAGTACTGGA GAAAAACGAG AGTGGATTTT TATGCCGGTG
20701 GGAATGAGGT AGGTGGGATT CTGAAGGTGT TTCTGGAGAG CCCTGAGGGC
20751 TGGGCCACGC AAAGGGCCTG CCTACACAGG GTGCTGGAGA CCCTCTGGGC
20801 ATGGATGCTG GCCAGGCAGG GGGGTGCTGG CATCCATAAA TGGTCTCCTG
20851 CGCCCTTCCA TCTTCAGTCA TATCTCATGG ACTTTTGCTG TTTTGTCTTT
20901 AAAGGTAAGT GCAGCAGGAG ACCCTGGCAC TCTCTGGAGA TGTCTGCTGG
20951 TTTGATTCTG GTCCCCGGTT GGGGCAGGAT GTGGCCAGGA CCATCGGGAA

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FIGURE 3G

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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21001 ACCAGCGCAG CCATGCTGGC CGTGCAAGGG CAGCTGAGCC TCTCTGTCCT
21051 GCTGTCTCTT CCAGGCGGGC GGGCACCACA GGCCCGAGTT TTCGTCTGCG
21101 CTGCAGAAGG CTCATGAGTT CCTGAGGCTC TCACAGGTGA GGCCGGTGCC
21151 TGGGGCTCTG AGGGGGCTGA AGAGGGGGAT CAGGGCTGGG AGCTCCTGCA
21201 GGCAGAAGTG CCCACCTCAC CTCCACCCTG CCCATATTTC TGCACCTGGTG
21251 TTTCAGGGTC ACCCCCACCC TCCCATCCCC TCCCTAGCCC CTGCTCCATC
21301 CACCGGTCCT CCTCGGCTG GCCTCACCTG GGGCAGTTCT CTGAGGCCTG
21351 CAGGGTGCTG GGGGTGCTGG CAGTTTCTGC GTCTGTCTCA TGTGGAGCC
21401 ACTGTGTGCA AGGGCCAGGC ACGGGCAGGG GCTGTGTACC CTGAGCTGCA
21451 CAGCCTACAC GGCACCTCCA TGTCTCTGAA GCACCTTCTG CCCATGGAGG
21501 TGACGCCAGC CTGTGGACTT GCCCTCCTGA GACTGTTTGC AGCAAAAGCC
21551 CCGGTCCCTC AGCTGCCTGC AGCTGCCTGC AGACCTGCC CGAGCCCATG
21601 GTTTGACCTC AGTGTCTCTC ACACGTGCCT GCACCCAGT CTGCAGCCAC
21651 AGTCATCCCA TACATGCGCC CCAACCTCCC GTGTCTCCCA CACCTGTCC
21701 CGGCCACGGC CTCAGCCAGT GTCCCTCTGC CTGGAACCGC TGCCCCCAG
21751 CCCCCTCTCC CTCCCTTCAG CTCTCACTAG GACATTGTTC TGCAGGGCTT
21801 CTGGGTCTTC CTGGCTCTG TGTGGCCAAG GCTGGCACCC ATCTTGGGCT
21851 CAAGCAGAGG AGGGGCATTG TCCTGTGTG CCTGGCCCAA TGGCGGCTG
21901 CTCCTGCTCC TGCCCTCTGC CCAGGACTTG CTCTGGGTGA TGGGGACTTG
21951 GGGAGGCTGA CTGAACCTTA CGGCACCTCA GGCCCTCTTC CTTCTCACTG
22001 AGGTGAGAGA GGCAGCCAGA AGCTGAGGTT GTTCAGGAGG CATTGGGGGC
22051 GCCTGGCACA GAGCACACCC GCAGAGACCT GGGCCCCCTC CCTGCCTTCT
22101 GGCCGGTGGG GAGATCACAG GGGAGTCAGG TGCTGACTCC CAGTCCCGTC
22151 TGGGCTGGTT TGAGCCCTCG CTGGCCAGTC ACCTTTCCCA GCAGCTGTGG
22201 GTGGTGAGCT AAACAGGTGC AGGCCCTCGC GCGCCTCGCA GCACCACTGG
22251 TGGCTGTGGC CGGCAGAGTA AGCTCCAGG CACGTTCTGC CTCTCCAGTC
22301 CTGCCCAGTC TGTCTCAGCG ATGTCCAGA TGGGGACGTC CCGTGGTGAC
22351 GTGTTCTCTG CTTCCACATT TGCCCTCGAT GCTGCCAGG TCCCAGATAA
22401 CCCTCCCGAC TACCAGAACT ACTACCGCCA GATGCGCAAG GTATCGGGGA
22451 GCCAGCCCCA TCCCTGTCCC GTCCCCCAGG GGAGGCCGCC CTCAGCAGGG
22501 TGGGTCCTTC CCTCTGAAGG GGGGGCTCCT CCCTGGGGGA CTCCTCCCTT
22551 GGCGTTTGTG GGTGTCCTGC TGTGTTGGAT GCCTGGCCTA GGGGCTCATG
22601 CTTTCATGTT CTGAGCTGCC TGGCACATGG AGGCACAGTT GGCTTGACAC
22651 CACAGCCGTG CCTCAGAGCA GTTCCAGTGG TCACGGCACA CACAGGCTTC
22701 AGAAGGACAG CCGAAGTGTA GCCAGTGTGT CCGGGGAAGG CAGAGGAAAG
22751 AAGTAGACCT CAGAGCCGGT GTGGGCTGTG ACCACAGGTG CAGACTGTGA
22801 AATTAGGCAT GGACCCAGCT GCTGCTGCCT GTTTACAATG GGGGTGGGGG
22851 GCACCTGGGC CCATCTCTGT CCGTCGTGAG ATCTGCAGGT GTTGAGGGTG
22901 TGAGCTGCAC CCCTGAGGGT CCCTGTGCTG GAAGCTGGAG GTCTGTCTGG
22951 ATGTACCCAG CTTGGGGCCC TGGCTGCACC CACACCTTTG GTGGCTGGGC
23001 CCCTGCCCTG ACCGGGTGCT CTGTGGTGGG GAGGGATGCG TCGGCTGTG
23051 GGGAGGTTCT GAGAACTGGG GTGTGGACAC CCCCAGCCTG GAGTCATGGC
23101 TTGTGCTCTG CAGGGTGGCT TCTCCTTCAG TACGCTGGAC TGCGGCTGGA
23151 TCGTTTCTGA CTGCACGGCT GAGGCCCTGA AGGCTGTGCT GCTCCTGCAG
23201 GAGAAGTGTC CCCATGTCAC CGAGCACATC CCCAGAGAAC GGCTCTGCGA
23251 TGCTGTGGCT GTGGTAAGGC TGTGGTCCCA GCAGCCCCGT CCATACCTCG
23301 TGTCTGTCAG ATGAGCTGCG TGCTCACTTC CACTCCTGTG GGCTCCAGCC
23351 CAGCACACAG TCCGGCCAGG CCGTAGGAGC TTGTCTTGG ATGGTGCTTA
23401 TATGTGGAGA ACTGTGAGCT CTGGCTGGAC CCTAGGGGC CTTGCTGGGC
23451 TGTGTGCACA GGGCCCTGCA CTGCGGAGCT GGTGTCCAGC CCAGCCACCG
23501 ATACTTGGGG GAGCCGCGT GGCCCCAAG GTTCTCTCT GGTGGTTTCC
23551 ACTGGGTGTC TGAAGAGGGA ATTTGTTGGT GTTGGTTTGG GTGCCACATC
23601 CTTTCAGCAC ATCTGGCTTT TGTGTGTGTT TCCCAGTGGA GACCTGCCCC
23651 TTTTCTGGCA GCACAGACTT GGTTTCTAAG TCATGGGCAC GTGTGGGGGC
23701 ATGTTCCCTG GTGGCTGTGC ATGGAGCCCC TGACAGATGA GGTGTCAGCT
23751 GCTGCTTGGG GCACCCGAGG GCTTGGTTAA CGTGGAAATC AGCTCTCCGC
23801 CCCCCTGTTC TGCCCCATCG GTTGTACAGC CTAGTGTGTC CTCTAGAGAG
23851 TTCCGCTGTG CCCTGGCGCG CTGTGTGTGC TCAGCACATG GGCGAGTTCT
23901 AGGGTGCTCT CTGTGATTTC AGCTGCTGAA CATGAGAAAT CCAGATGGAG
23951 GGTTCGCCAC CTATGAGACC AAGCGTGGGG GGCACCTGCT GGAGCTGCTG

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FIGURE 3H

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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24001 AACCCCTCGG AGGTCTTCGG TGAGTGGTCG GCCAGCACTG CGGCGCGCAA
24051 ACCCGGGGCT GGCTAGCACT GTGGTACACA AACCTGGGGG CCAGCTTTTC
24101 CCCCTTGCCC GAGGCTGCAA GGGCCCAGGT TCACCGGCAG ATCTGTCTGG
24151 AGCCCTCCCT CAGCCCAGGC TGTTCTGCGC TCCTCCATCC CCCGGGGTGG
24201 CAGGATCCCT GTGTTGTGGA TAGGAGGGCA TCAGGTGAGA CCTAGGGGAC
24251 AGTGGAGGGT TCCAGTGAGA TCCACAGCCT GGGCTGGTTC CTGCTCAGTC
24301 CACAGGCTT GTGTTCTGTG GAGGCTGCTG TGTATCCAGA GCGCCTGCAG
24351 GGAGGTGTCT TTGGGGACTG TGGGGACTGT GGGGACCCAT GCCATGGGCA
24401 GTAGGCTGCT GTGTGTGCAT GGTTCGCCACC GTACTGGTCT TGGGGGAGGA
24451 TCTCAGCCCT GGTCCACCTC TGGGCACCTC ACATACCCGC CTTCTTGGTC
24501 CCCTCCACAT CACACATGGC TTTTGGGGT GGGGTGCGAG CTTTCTGTCTG
24551 TGTTCCCTC ATCTTCGCTC TCAGGTAGCA CAGGTGTGTG TCCTGGACCA
24601 GCCGGCGTTT GCTCTGGAGG TTGGTCAGGG AGGCAGCGTC CGGGCCCGGG
24651 CTCACGCAA CACTCTTGCT TGTTGTGGCT TTGCCTGAGC TGCAGAGCCT
24701 GGGCAGCCAG GGTGAAACCC AACACTTGGT TCTTCCCTCC CTTTCCAGG
24751 GGACATCATG ATTGACTACA CCTATGTGGA GTGCACCTCA GCCGTGATGC
24801 AGGCGCTTAA GTATTTCCAC AAGCGTTTCC CGGAGCACAG GGCAGCGGAG
24851 ATCCGGTAAG GAGGCTCTCA GCCATTGAGT GTGGGCGCTG CCAAGTCGGG
24901 GGCCAAGACC CAGACGCATC ATTCTGTGAC ACGGCCCTGG TGGCCATCT
24951 CAGAAGCGAA ACTCATGGAA ACATGCAAGA GGCTTCGGAT GTTGTGGAAT
25001 CCAGTCATAT GCCCTAAAGC ATACAAAATA TCTGTAGGG GCTCAGAATA
25051 GCACAGTTAT GATACAAAAA TGGATTTTCT CTCTCTTTTA ATAATGTTAA
25101 GAAGACATCA CATACTGAC TCCACCGGTG TCCCAGAAAC GGTTTTAAAG
25151 TAACCTTTCC TGTTGAAGGG TAGCAAGTAT TCAGAAAAGT GTACAGGTTG
25201 GTCTTCTTGA AGCAAACAGG AAGCGAACAG TGCCAGCATT AGACATGGTG
25251 ACACCACCAG AGCCCTCGGC CCGCCCCATG ACGGGGCCGC CCACATGCCT
25301 GCCAGGTGCT GGGTGTCTGT TGCTCGCTTT GGATCTTGTC TAGGTGGACT
25351 CCTGAGGTGT GGAATTCGTG TTGCCTTCTC CTGCTCTCCT GCTCTCCTGC
25401 TCGCGGTTAG TCAGGTGGCT CGGGTAACAG CAGCGTTCTC TCCCTCGGGC
25451 CTTGCGTTGA ACACAGAATG CCGCGCTATC CAGCTGCCTG TTCTCAGCAC
25501 CTGGGAGGAT TTCAGTCTG GTTATTATGA AGCATCTACT GTGAACACTC
25551 TTGTACTTAT CTTTTGGGGG CACCTGGGTA CCCATTCTC ATGGTCACGT
25601 ACCTAGGAGT GGCATTGCTG TGTTAGAGGG TACGTTATAG GGTATGTGAT
25651 TTTTGTAGGT TCTTCTTTAT CCTATCACGA TTACATTTT TTACTTTTGT
25701 TCAACCTGGT GTAGACTCAC CTTGGTCACA ATGCACTGTC CTTTTTATAT
25751 ATTGCTAGAT TCAATTTGAA GAATATTTT TTAGGATTT AGCAACTCTG
25801 GTTACAAGAG ACGCTGGTCT ATAATTTTT TTTCTTTATA ATGTTTTTGT
25851 CAGGTTTTTC GTTAAAGATG ATGCTGGACT TAGAAAAGCA GTTGGAAAAT
25901 GCTTTTAAAA TACTCTTTGG AAGAATTTAT GTAATATTCA TAATATTTCT
25951 GCCTTAAATG TTTGGGAAAA ATTACCGGAA ATGCCAGTTG GGCTTGGAGA
26001 TTTCTTTGAG GAAAGTTTT AAATTAGAAG TTCAATTTCT TTCTTTCTTT
26051 CTTTCTTTCT TTTTTTTTTG AGATGGGTTC TAGCTCTCTC ACTCAGGCTG
26101 GAGTGCCTGT TAATTTCTTT AATAGTTTAT AGGACTGAGC AGATTTTCCA
26151 TTTTGTATC AGTCTGGGGA GTCTTCCCAT TTCCACTCAG CTTTACTCTG
26201 ATTCATGCAA AGTTGTTTCA TGTCCTCTTA GATGGCTCTG AGCCCAACGC
26251 TGACATCCTC CTCTTCTTTC TGAGAATCTT ATACTGATCT TTTGAAAAAA
26301 AAAAAATCTT AGTCTTTGAT TCTGTTTTTA AAGAGACTTT ATTTTGGTT
26351 TCATCAATTT CTATTGTTTG TTATTTTCTT TCTTCTTAA TTTTTTTGAG
26401 ATGGAGTCTT GCTCTGTTGC TGAGGTTGGG GAGCAGTGGC GTGATCTCAG
26451 TTCACGCAA CCTCCGTTTC CGGGTTCAA GCGATTCTCC TGCCCTAGCC
26501 TCCCAGTAG CTGGGACTAC AGGTGCTGAC CACCATGACT GGCCAAATTT
26551 TTGGTATTTT TATTAGAGAC AGGGTTTAC CATGTTGTCC AAGCTGGTCT
26601 TGAACCTCTG ACCTCAGGTG ATCCACCTTC CTTGGCCTCC CAGAGTGCTG
26651 GGATTACAGG TGTGAGCCAC CACACTGGCC TTTGCTATTT TCTTCTCCT
26701 TTATTTTCTT AACTTGAATA CTTAGATATT TGATTTTCAG GCTTTTATTG
26751 AAATATGAAT TTGAGGCTAT AAATGAGTTT TGAGATATCA TTCAGTTAAA
26801 TGTGTGTTCT GGTGCTTGCT GTGGTAGCAC AGATACTAAA AGTGTTTTCT
26851 GTTCTTACTG TTCTTCTCTG GCCCATGAGT TATGTGGGAG TATGCTGCTT
26901 CATTTACAAT CTGAGAATGT TCTGGTGTGG TTTTTTTGGA AGCCGTGGAT
26951 GGAGCAGGGG TTTTCTTGTG CTTACAGGT GCAGCTAGGA GGGCACTGTG

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FIGURE 31



Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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27001 TCCAGGCTCT TCTGTCGGCC TGGCGTGGCC CTTGGCCATG TGCTGCTCTG
27051 CGGCATGAGG TGGGCGTGAG TTGTCTCAG CCACATTTAG AGAATTGGCC
27101 TTTTAAAAAA TAGATCATCT TTTAAAAATC ACTGTAATAA AAGTAAAGCA
27151 GGTTCCTTGC AAACAAGACT TGCAAAATAC AGAGAAGCGC AAAGAAGAAG
27201 CTAAGTCGCC CCTCCTCGCC CCTGAAGGAG AATCTGCTGT TGCTGTTTGG
27251 TCTCCACATT TCCATGGCGG CTTGCTGCCC CTTTCACGCC TGGCCCACTT
27301 TGTGCCTGGT GAGGTTTCTA AAAGCCCCAC CCTTGAGCGC GTCCTCCAG
27351 CACGAGCAGT AATGGCACAG GTGTTGTGTC ATTTTACTCA GTAGCCTCTG
27401 GGTTATTTTT CAGTTTTCCT TGTTGTTTTT TAGCTTTTCC CCATTTTAAC
27451 CTTAACTGGT ATTTTCTTGT TAAATATTTA TTCATGACCA TTATTATTCC
27501 CTAGAGCCAC ATGGCTTGGG GTCCACCTGC CTGGGTCCGC CCCCATCCCT
27551 GCCCCTTCTG CTGTCTGAC CTGGCCTGGT GACTTCTCTT CTCTGCTCAT
27601 CTCTCTCCCT GCCTGAGTGG GCAAGAGTAC AGCCTCACAG AGTGGTGGA
27651 TTGTGTGAGA TGCCACAGGG AAGCACATGT CAGTTGTTGT CACTGTGTAG
27701 AACAATGAGT CCCGGATGTG GCCCGCAGGG GAGCAATGGT GACTTAATCG
27751 CGGGCTTCCT CTGCATTTCT TTGGTGACTT CCAAGCTAGA ACATTCTTTT
27801 TTTGTTTATT TGTTTGAAGC AGGGTCTCAC TCTGTTACCT AGGCTGGAGT
27851 GCAGTAGCAA AATCATGGCT CACCACAGTC TCAAACCTCC GGGCTCAAGC
27901 AATCCTCCCA CCTCAGCCTC CTGAGTAGCT GGGACTACAG GTGCATACCA
27951 TCACCTGTGG CTAATTTTTT AAATGTTTTG TATTTTTTAA ATGTTGCTCA
28001 GGCTGGTCTT GAACTGCTGG GCTCAAGCAA TCCTCCACC TCGGCTCCC
28051 CAAATGCTGG GATTACAGAG TGAGCCACCA CACCAGCCA TTTTAAAAAT
28101 TTTCACCAGG AAGTTTTTTT TTTCATTTTT AAGCACAGTA AGTATTTGTG
28151 TATTATGTTA CAGATATTTT CCCCTCAATT TCTTTGTCTT TTTTATCTCT
28201 TTAGGGAGTA TGAACATAAG TTTTAACTT TTAATGGTT AAATATATTA
28251 GTGTGATTTT TATATTAAGA TTTTATTTTA TTTATTTTTT TTTTTTTTGA
28301 GACGGAGTCT CGCTCTGTCG CCCAGGCTGG AGTGCAGTGG CGGGATCTCG
28351 GCTCACTGCA AGCTCCGCCT CCCGGGTCA CGCCATTCTC CTGCCTCAGC
28401 CTCCCAAGTA GCTGGGACTA CAGGCGCCCG CCACTACGCC CGGCTAATTT
28451 TTTGTATTTT TAGTAGAGAC GGGGTTCAC CGTTTGTAGC AGGATGGTCT
28501 CGATCTCCTG ACCTCGTGAT CCGCCCGCCT CGGCCTCCA AAGTGCTGGG
28551 ATTACAGCG TGAGCCACCG CGCCCGCCT ATATTAAGAT TTTAACTTG
28601 CCGGGCGCAG TGGCTGACGC CTGTAATCCC AGCACTTTGG GAGGCCGAGG
28651 CGGGTGGATC ACAAGGTCAG GAGATCGAGA CCATCCTGGC TAACACGGTG
28701 AAACCTTGTC TACTAAAAAT ACAAATAA GCGGGCGGTG GTGGCGGGCG
28751 CTTGTAGTCC CAGCTACTCG GGAGGCTGAG GCAGGAGAAT GGCGTGAACC
28801 CGGGAGGTGG AGCTTGCACT GAGCCGAGAT GGTGCCACTG CACTCCAGCC
28851 TAGGCGAGAG TGCAAGACAC CGTCTCAAAA AAAAAAAGAT GATTTTAAAC
28901 TTACCTGGAG AGTTTTTGAG ATACAGTTTG GAGTTGCAAG TTACTTTAAC
28951 ACTATTTATA TGGAATATTC TATTTTACTA GACAGACTTA AATTCTCCCT
29001 TAAATTCACA AATTTATAGA AAAGTTACAA AAATACTGAA AAGTGCTCCT
29051 GTTTACTCTG ACTAGAATTC TTTAGTGGGT GGCACCCTAC CCTGAGGGCT
29101 TCATGACCTG TCCTCCACCA TGATCCAGGC TCTACCCTCA GGGCTTCATG
29151 ACCTGTCCCT CCACATGATC CAGGCTCTAC CCTCAGGGCT TCATGACCTG
29201 TCCTCCACAG TGATCCAGGC TCTACCCTCA GGGCTTCATG ACCTGTCCCTC
29251 CCACATGATC CAGGCTCTAC CCTCAGGGCT TCATGACCTG TCCTCCACAG
29301 TGATCCAGGC TCTACCCTCA GGGCTTCATG ACCTGTCCCTC CCACGTGATC
29351 CAGGCTCTAC CCTCAGGGCT TCATGACCTG TCCTCCACAG TGATCCAGGC
29401 TCTACCCTCA GGGCTTCATG ACCCTTCCTC CCACATGATC CAGGCTCTAC
29451 CCTGAGGACT TCATGACCTG TCCTCCACAG TGATCCAGGC TCTACCCTCA
29501 GGGCTTCATG ACCTGTCCCT CCACATGATC CAGGCTCTAC CCTCAGGGCT
29551 TCATTACCTG TCTTCCACCA TGATCCAGGC CCATTCCTTT TGAACCAT
29601 GGAAAGGAAT TTGCAGATAG GATGTGTACC CCTAACTGCC TGAGTATTTT
29651 TTAGCAGGTG TATTCCTTTG TGCAAGTGTA AGTCAGAATG TTAATGTTGA
29701 TGAAATACTA ATCTGCAGGC CTAATTGTTC CAATAATGTC CTTTATGGCA
29751 AAATCTTCCC CTCAAGCTTT AATCCAATAT CATGGGTTGC ATTTGTTTAT
29801 TTTTAATTAT TTTTCTTTT TTTTCTGTT TTCTTACCC TTCTCACTGT
29851 GCACATGGT TGCATTTAGT TATCACATTG ACACCTTTT AACCTGGAAT
29901 AATTCCTTAA TCTTCCCTTG TGTTTGATGA CTTTGTCAAT TTTGAATTGT
29951 TCCACAAGTT ATTTTGTAGA ATATCCTCAG TGTTTTTTTT TTTCTGGTGT

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FIGURE 3J

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30001 CTCGTGATTA GATTTCAGGTT ATGAAACTAC ATTTTTGTCA GGAAGATTGC
30051 AGAAGAAATG GGGCCTTCTC CTGCACCTTA CCAGGAAGCA CACACCAACT
30101 TTGATCCCTT GATTAAGGTG ATGACCGCTG TACTTAGTTT CTCCGCTATG
30151 AAGTTGCTTT TTTTTCTTTT GTGGGGAGAC AGTTTTAGAC TATGTAAACG
30201 TCCTATTTCT CATCATACTT ATACCTGTTA GTGTTAGCAT TTGATGATGA
30251 TTCTTGCTG AATCAATTAT TTGCATAATG CTTACAAAAT TATCATTCCT
30301 TCCATATGTA TTAGTTGGTG TTCTTCCAAA AGCTTTTCCT TTGCCCTCTGT
30351 TTATTTACTT ATTTTACTACT GTGGACGCAT AGATTCTTAC GCAATTGATT
30401 TTGATACTGA TCTCATAGCT AGACAATTTT GCTAAACTTT TAAAAAATT
30451 TATGTACTTT ATCTTTTATA GCAGCTTAA ATTTACAGAA AATTTGAGTG
30501 GAAGATGTA TGTTCCTATA AAGCCGCTAA CTCCTCGCAC CTTCCCTCAA
30551 GTTTCCCCAG TACTAACATC TTGCATTCAA GTGGTGCCTT TGCAACATTC
30601 ATAAATTATT ATCGTCCAGA GTCCATTGTT TACATTCAGC TTCTCTTCA
30651 TGTTGTTTCT TCTGTGGTTT CACAGATGTG TGATGCATGT GCCCACCCT
30701 GCAGTGTGAC ACAGGATCTC ACTGCCCCGG AGTCCCTCTG GCTGTCCCCG
30751 CCTCCAGAAC CCCTTAGTAG CAAACACTGA TATTTTACT GTCTCCATAG
30801 TTTTGCCCTT TCAGACTGAC CTATTTCACT TAGTAAGAAG CATTTAAGAT
30851 TCCTGAGTCT CTTTCTATGG CTCAATAGCA CATTCTTTT TAGTGCTGAA
30901 TAATATTCCA TTGTCTGGAT GTACCACAGT TTATTCATT ACCTACTAAG
30951 GTGAATGTCT TGCTTGCTTC CAAGTTTGG CAACTATGAA TAAAGTTGCT
31001 ATCAATGTTA GCGTGCACAT AAGTTTTCAG CTCATTTGGG TAAATGCCAA
31051 GAAGCATGAT TGCGGGATCC TATGGTAAGA GTGTGTTTAG TTCTGTAAGA
31101 AGCTGCCAAA CTGTATCTTA AGTGGCTGCA CCATTTGCGT TTCCACCAGC
31151 AATGATGAGC GTTTTGTGTC TCCACATCCT CACCAGCATT TGCTGTTGTG
31201 TTTTGGGTTT TAGCCTTTCT AAGAGGTGTG TAGTGGTATC TCCTTGTTTC
31251 AATTTGCAAT TCCCTAATGA CATTATGTTA AAATCTTGTC ATATAGTTAT
31301 TTGCCATCTG TGTATCTTTT TCAGTGATGT GTCTTTTAAA GTCTTTGGCT
31351 CATTTTAAA TTAAATTTTC TTATTGTTGA GTTTTAGTTC TTCATAATT
31401 TTGGCTGCCA GTCTTTTATC AGATATGTCT TTCGCAAATA TTTTCTGCCT
31451 GTGTCTTGTC TTTTCATCTT ATTAACAGTA TCTTTTGAGC AGCCAGTTT
31501 CATTTCAGG AAGTCCAGCT TATCAATGTT CTCTTTTATG TATCATGTTT
31551 TTGGTGTGT ATCTAAAAAG TTAGTGCCAA GCCCAAGGGT ACCTAGATTT
31601 TTTCTGTGT TATATTCTAG GATTTTAAA GTTTTGCATT TTACATCTAG
31651 GTCCATGATT CATTTTGAGT TAACTTTTGT GAAGGGTTTA TGGTTTGTGT
31701 CTAGATTTT TTTTTTTTTT TTTTTTTGCA TGTGGATGTC CAGTTGTTT
31751 GGTACCATCT GTCAAGAAGA CTCTTTTGG GTCATTTTGT TGCCTTTGT
31801 TCTTTGTAAA AAATCAGTTG ACTGCATTG CATGGGTCTA TTTCTGAGCT
31851 CTCTGTTCCA TTGCATTGAT CTGTTTGTTC TTCTCAGCAA TCCCACACTG
31901 TCTTGGTTCC TGTAGCTCTG TAGTAGGCCT TGCAGTCAGT TACCGCCCT
31951 GTTCTCACTT CAGTGTCTC TTCAATAGTG TTTTGACTAT TCTAGGTTT
32001 TTCCCTCTCC ATATACATTT TAGAGTCAGT TTGTCAATAG TTTACAAAAT
32051 AACTTGCTGA GACTTTGATT GGGATTACAT TGAATCTGTA GCTCAAGTTG
32101 GAAAGATCTT TTATTTCTTT CATCAGAATT TTGTAGTTT CATCATATAT
32151 AGATCTTGTA CATATTTTGT TGTTTATACC TAAGGATTCT ATTTTTTTGG
32201 TGCTAATGTA AATGGCGTTG TGTTTTAAAT GTCAAAATCT AATTGTTTCT
32251 TGCTGGTAGG AAAACAACAG ACCCTTTTTC TTTTTTTTAA GGGACGCAGT
32301 CTTACTCTGT TGCCCAGGCA GAGTGCAGTG GTGCCATCAT AGCTCACTGC
32351 AGCCTCAAAC TCCTGGGCTT AAGGAATCCT CCTGTCTCAG CCTCCTGAGC
32401 AGCTAGGACC ACAGGCATGT GCCACTACGT TCAGCTAATT TTTCAATTTT
32451 TTTGTAGAGA TGGGATCTTG CTCTGTTGCC CAGGCTGGTC TCAAACCTCC
32501 GTCTGCTTTG AGATGATTAT ATATTTGTGT CTTTGTAA TTTAGAGGAT
32551 TATTATGGAT TTTTCTAATG TTAAGACACC TTTGTATTTC TGAGATCGAC
32601 CTTAGTATTG GTCTATATTT AAGACAGTAT TCAGTTTCTC AGTTGTTTTC
32651 TGTTTTTTTGG TTTTTTTTTT TGAGACAGAG TCTCTGTCTC CCAGGCTGGA
32701 GTCCAGTGGC ACAATCTCAG CTCACCGCAA GCTCTGCCTC CCGGATTAC
32751 GCCATTCTCC TGCCCTCAGCC TCCCGAGTAG CTGGGACTAC AGGCGCCTGT
32801 CATCATGCCC AGCTAATTTT TTGTATTTT AGTAGAGACG GGGTTTCACC
32851 ATGTTAGCCA GGGTGGTCTC AATCTCCTGA CCTCGTGATC TGCCACCTC
32901 GATCTCCCAA AGTGCTGGGA TTACAAGGCG TGAGCCACTG CGCCCGGCAG
32951 CAGTTTCTCA GTTTTAATTT GGAGTTTTC ATCTGTGTTT ATGAGTGAGC

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FIGURE 3K

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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33001 CTGAAATTTT CACTTTTCCA TATCTTATTT CTCTGGGTTT CTAGAATGAG
33051 CTAGAGAGTG TTCCTCCTTT CTGTTCTCTG GAAGAGTTTG TGTGAGATTA
33101 GAATGAGTGT GTCTGATAAT TTAGTTGCAT TCATTTATAA AATTCCTAGG
33151 CCTAGAGTTT TTTTCTGGG AAAAGTTTAC ATTTTGACTC ATTTTTTTAG
33201 TAGTTTTAGG ACTGTTTAGG TTCTCTATTT CTTGATTGAG CCAGTTTGA
33251 TAAGTTAATC TTTCTAATTT GTAGATATTT TCTCTAAGTT TGCAAATGTA
33301 ATACATAAAA CTTTCTTGTC ATTTCTCACC ATATCTGTAG TTCTATCTTT
33351 TTATTGCTAA TATTACTAAT TTGTACTTTG ACTATTTGTA TTTGTTACCT
33401 GTTGCCGAGT AACAAATATTA GTACAAACCT AGTGCGTTAG AACAAACACAC
33451 ATTGATTACT TCACCGTTTC TGTGTGTCAG AAGTCCAGGC GCGGCCCTCGC
33501 AGGTCGTCTT CTGCCCTCAG GTCTCTCCGG GCTTCAGTCA GGGTGTTAGC
33551 CAGGACCGGG GTCTCGCCTG AGCTTCCAGT GAGGAAGGAT CTGCCTCTGA
33601 GCACACAGGG TCCTCGGCAC GATCCCATTG CTCAGCTGGA AGCTGCCGAC
33651 TGCCGTCTGC TGCGGGGCCT CTCTAGATGG CATCTTCACA AAAGCGAGAA
33701 GGGAGAGTTG GTAGAGGGAG TCTGCTAGCA CCATGGGAGT CGCGGTCACA
33751 CAGACCTCGG TCCCAGGACC CGCACCCATC AACCTGCGG TGATCTGCTG
33801 GTTAAAGACA AGTCCCACGT CCCACAGGGT GACACTGGAG TAGACACTTC
33851 GCTCTGGCCT TTTAGAGAA CTGGTTATTT TTTGGAAATA TCAGTTAGAT
33901 GTAGGATGGG TCTTGTCTTC TAAATCTATT GTTTTCTCTC TAATTGATTT
33951 TTTCTGTTT TTATTTAGTT CACTTTGTTG GGTTTGCTCA AGCCTGGGTC
34001 ACTGGATCTC AGGGATGCTG CTCTGTTTGG CAGCTGTGTC TGCAGGGGCT
34051 TCCCAAGGCC TTGCTTTCCC CTCACGTCCC TTTCTCAGAC TCTGCCAATC
34101 CGCTTCCCGC TCTGGTGTCC TGTGGTTGCT TCTTTTAAA ACCCTCATCG
34151 GTCTGTGTAA ACTGTTTATT TTTATGTGGT TTTTAAGGGA GACCATTCTC
34201 ATTCTTTTGA GACCCCTGAA AGGATGGAAT TGGGATAGGT AAAGTGTCTG
34251 TTTACCAGAA TGTTCACCTG ACCAATCTCG TGTTCAGGG AGACCCTCAC
34301 GCAGGGCTTA GAGTTCTGTC GCGGCAGCA GAGGGCCGAT GGCTCCTGGG
34351 AAGGGTGAGT GAGCCTCCAC TCGTGAGTGC AGAGATGCAT GGGATCCAGA
34401 GGTTTCTGCT CTCACACACT GCGTTCATAA ATGTTGGCTT GTATGTTGTT
34451 GCTACACCAG AAGTTTCTGG AAGTGAGCTG CCAGCCCGTG ACTTCTGGGG
34501 GACCTCGTTC CTTTGTGGCA TCGTGCGCTT TTGCCCCGTT GGAAATTGCT
34551 CAGTACGTTG CCGGGCCGAG CCGGGCTGCT GGGAGCGCGC TGTAGCCTGA
34601 GCGTGGCTAT TCCCTCCACC CTTTCTGCTT GCTCTTAGGG TCCAGCAGAC
34651 AGAGCTGCTG TCTTCCACGG CCTTAATGCC TGAGGCACTG GAGTTGGTGG
34701 GCTGGCTGGG GCACGTGTGA TTGTTGCAGA ATGCGTGTG TTTACACACAC
34751 CGGCTGTGAA CAGGGTGGAA GGGCTGAGGC TCTCCCTGTT TCCCTCCAGC
34801 TCCTGGGGAG TTTGCTTCAC CTACGGCACC TGGTTTGGCC TGGAGGCCTT
34851 CGCCTGTATG GGGCAGACCT ACCGAGATGG GTGAGTGAGT GCCTGTCCCTC
34901 TGGTGGGTGG GGGTTCCTAA CCCAATGCTC TGTGATGAGT GTTTTGTGCT
34951 TTGACATTTG GTTTTAGGGT TTGTTTGTGTT GTTTGTTTGT TTTTGAGACG
35001 GAGTCTCGCT CTGTCAACCG GGCTGACATG CAGTGGCATG ATCCTAGCTC
35051 ACTGCACTCT CAAACTCGTG GGCTCAAGCG ATCCTCCCGA GTAGCTGGGA
35101 TCACAGGTGC ACGCCACCAC CCCGGGCTAA TCTTTTAAA CTTTATGTA
35151 GAGATGGAGT CTTGCTGTGT TGCTCACACT GGTTTGGGCT CAAGCAGTCT
35201 TCCTACCTCG GCCTTCCAAA GTGCTGGGGT TACAGGCATG AGCCAATGTG
35251 CCTGGCCTGT TTTTAATATT TTTAAACAGT GAGATAAGAT CCCCAGTTGA
35301 AATGAAGATG TTTCCCTGGT CCCACAGCTC TCTGGAGCTT CCTGACATGT
35351 ATGCTGGAGG GACGCTTCTG GTCTCCGGCC CTTCCAGGCA TACAGATGCC
35401 TCCCAACCCT GAGTAGGAAG ATTAGGCTCC ACGGCTCGC TGGAGCGGGT
35451 TAGAAGGCAG GAGATCTCCG GTCCAGCCG TGTCTCCAGC CGCCGACTC
35501 TCTCCAGCC CTGCTCCAG CTGCCCCACT GTCTCCAGC GTCTGCCGTG
35551 TGGATGTTTA GAGGTGGGGA GCACCGTCTG TGGCTGAGTG CAGCTTGTGA
35601 GACGCTGCTC CCAAGCACTG CAGACCTCAC TCAGCCTGAC GCGTCCGTGA
35651 GGCCATCCTC GGTACTCGCA TGTCCCTTTG TCTTCCAGC GACTCTGGGA
35701 GGCAGGAGTA TCTGTTCCCA GTTCACATCT GCAAAAGTCA AGCTCGGGTT
35751 TCAGTAGTGG CCCATGGCCC TTAGGTAGGG TGGCCCCATC GTGCAGGCTC
35801 CTCCCCGTAC CCAAGGCAG CCTGCTGGGG TGAGAAGCCA GGGGCTGGG
35851 ACCTTCCTTG GTGTGATGGT GTCTCTGTCT TCTGGTCTTT GCAGGACTGC
35901 CTGTGCAGAG GTCTCCCGGG CCTGTGACTT CCTGCTGTCC CGGCAGATGG
35951 CAGACGGAGG CTGGGGGGAG GACTTTGAGT CCTGCGAGGA GCGGCGTTAT

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FIGURE 3L

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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36001 TTGCAGAGTG CCCAGTCCCA GATCCATAAC ACATGCTGGG CCATGATGGG
36051 GCTGATGGCC GTTCGGTGGG GACGACGGGA CCGTCCCTGA GCCTTGGGTT
36101 TGGGTAGAGG AGGGACACTC AGCTGTGAGC CCGTGGCCTG GGCTGAGTGA
36151 ATGTAGAGAG GAGGGGAGGC CTGTGGGCCA GGTGAGCTGC CACTCTGGGA
36201 ACAGACACCT ACAAGAGCCA CATGCCTGGT TCCTGGGGCA AGAACGTGGG
36251 CTGCTCTGAC CAAGTGGGGC CCTGCAGAGA GGCTCGCCTC TTAGAAGTGA
36301 ACCACCCACC ATTAGCCATG TCAGTGAAG AGCAAGCACA TCAGGGACCC
36351 ATGGAACAG CGAGGTGGGC TGCGATGAGG ATGCTGCTTC CTGGTGTGGT
36401 AGTGATGACG GTCACAGCAG CTGCTCTCTG TGGCCCTACT GTGTTACAG
36451 CTGGTGCTGA GCCACATATG TGCCAGGTGC ACACACACGC AGACGCATGC
36501 AGGCAGGCAT CAGTGTACAG ACTGATGTGC ACACACAGAT GTACATGGAG
36551 ACAGATCACCT ACACAGGCCT ATGCACACAC GTACGCATGC CCACACAGGC
36601 ACCTGTGTCC ACACACATAC AGATGCACCC ACAGCATCCC ATCTGTGCCA
36651 CACACTGACA TAGGTACATG GAGACAGATG CACACACAGG TCTGTGCACA
36701 CACGTATGCA TGCACAGGCA CCTGTGTACA CACAGGTACA GATGCACCCA
36751 CAGGATCCCA TCTGTGCCAC ACACAGACGT AGGTACATGG AGACAGATGC
36801 ACACACAGGT CTGTGCACAC ACATACATAC GCATGCACAG GCACCTGTGT
36851 ACACACATGC AGATACACCC ACAGCATCCC ATCTGTGCCA CACACAGACA
36901 TAGGTACATG GAGACAGATG CACACACAGG TCTATGCACA CACATACGCA
36951 TGCACAGGCA CCTGTGTACA CACACGTACA GATGCACCCA CAGGATCCCA
37001 TCTGTGCCAC ACACAGACGT AGGTACATGG AGACAGATGC ACACACAGGT
37051 CTGTGCACAC ACATACATAC GCATGCACAG GCACCTGTGT ACACACACGC
37101 AGATACACCC ACAGCATACC ATCTGTGACA CACACAGACG TAGGTACATG
37151 GAGACAGATG CACACACATG TCTGTGCACA CACATACATA CGCATGCACA
37201 GGCACGTGTG TACACACATG CAGATACACC CACAGCATGC CATCTGTGAC
37251 ACACACAGAC GTAGGTACAT GGAGACACAT GCACACACAG GTCTGTGCAC
37301 ACACATACGC ATGCACAGGC ACCTATGTAC ACACATGCAG ATACACCCAC
37351 AGCATCCCAT CTGTGCCACA CACAGACATA GGTACATGAA GACAGATGCA
37401 CACACAGGTC TATGCACACA CGTATGCATG CACAGGCACC TGTGTACACA
37451 CATGCAGATG CACCCACAGT ATCCCATCTG TGCCACACAC AGACATACGT
37501 ACATGGAGAC AGATGCACAT ACAGGTCTAT GCACACATGT ACACATGCAC
37551 AGGCACCTGT GTACACACAT GCAGATGCAC CCGCAGTATC CCATCTGTGC
37601 CATAACAGCA CACACGTACA TGGAGACAGA TGCACATACA GGCTATGCA
37651 CACATGTACA CATGCACAGG CACCTGTGCA CACATATGCA GATGCACCCG
37701 CAGTATCCCA TCTGTGCCAC ACACAGACAT ACGTACATGG AGACAGATGT
37751 ACACACAGGT CTATGCACAC ATGTACACAT GCACAGGCAC CTGTGTACAC
37801 ACATGCAGAT GCACCCGAG TATCCCATCT GTGCCACACA CAGACATACG
37851 TACATGGAGA CAGATGCACA CACAGGTCTA TGCACACATG TACACATGCA
37901 CAGGCACCTG TGCACACATA TGCAGATGCA CCCGCAGTAT CGCATCTGTG
37951 CCACACAGAC ATACGTACAT GGAGACAGAT GTACATACAG GTCTATGCAC
38001 ACATGTACAC ATGCACAGGC ACCTGTGCAC ACATACATAC AGATGCACCC
38051 GCAACATCCC GTCTGTGCTG CCCTATTAGG TTTGTGGCCA TTTGGGGAAT
38101 CTTCTAAAA CCCTAAAAGC TAGGGCAGGT CTGCTTGAGC AGGAGCAGCA
38151 GGGTCTGGGG GACCCCTGAG GGCAGGACAG TCAGGGACCC ACAGTTGAGC
38201 TGGGCCCCGT GAGCCCTGGA TCCTTCTTGG TGTCTTATCC TGGCCAGCAA
38251 GCAAGTGTGA GCTCCTGTGG GTCTCCAGAG GCCCATGAGG ACCAGTGGGC
38301 CAGTTGGGAA CAAGGCTTGG CGTCCCTCTC AGGGGGGAAC ACCAGGGCAG
38351 GCCTGAGGAG GCCTGTGTCC CCAGCCTGTC ATTGCTGTGG CTCCGCTTCT
38401 CAGGGAGCCT AGGAAGAAGG TGTGGCAAGA GCCCAGGCG CTGGCTGCAC
38451 CTGGCGGGGC CTGTGGGCGT CAGTTTAGAC CCATCCATTC TCACTGCAGC
38501 ATTCAGGGT TTGCCCTTAT GCTCGGCTGT GTGAGGGTGA GGATGATGCT
38551 GTGGGGCGAT GCATGCTGGG TGTGTTTCAG CCTTCTCTTC CACCAGGCAT
38601 CCTGACATCG AGGCCCAGGA GAGAGGAGTC CCGTGTCTAC TTGAGAAACA
38651 GCTCCCCAAT GGCGACTGGC CGCAGGTATG CCGCCAGGGA CCTGAGCGCA
38701 CAAGGCCCAG CACTGACCTC CAGCGTGCAT GGCTGTTTCC ACGTCCCCCT
38751 GCTCTGTGTC CTTTTTGGGG TACTTTGGAC ACTTGGGAGG CGTCACCTCT
38801 GCCAGTGAAT GCCACAGTTG GTGGCAGGTC TGTGGCAGGT GGTCCGGTCC
38851 TAAAGTCCAG ATCTTGTGTG TGTTCAGT GATGCTCTGG GTGGGGGAGG
38901 AGCTGGATGG GAGAAGCCAG TGGGCGGAA GCCTTTTTCG TGCAGGACAG
38951 ACCCTCCCAC TCCAGATGAC CTAGTGGCCC CTCCTGAGC CAGAAGTCCC

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FIGURE 3M

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

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39001 TGTGGTGTGG GTGTCATGAG GTCATGTGAG GCCAACCGCC CTCCCCTGGG
39051 ATGAGGCTGA GTTGGTGGAA GCTGATGTGG TTGTGAGGGG CTGGTGACCC
39101 TGGCTTAGGG TTTGCTGCAG GGCGGGGAGT CTGAGCTGGG CTGATGGTGC
39151 CATGACTGAT GCGGGATGGA CTACTTGCTT TCCTATGCTC TTGCTTAATT
39201 AGCCCTTTCC AGGCTGACTC ACCCACAAGC CAGCCAAGCC AACAGCCAGG
39251 GCTCCAGTTC AGGGACTAGC CCTCAGCTGA CTGGTGAAGC CTTTGTGTTT
39301 ATTTCTCTGT GTTCTTTTAG GAAAACATTG CTGGGGTCTT CAACAAGTCC
39351 TGTGCCATCT CCTACACGAG CTACAGGAAC ATCTTCCCCA TCTGGGCCCT
39401 CGGCCGCTTC TCCCAGCTGT ACCCTGAGAG AGCCCTTGCT GGCCACCCCT
39451 GAGAACATGC CTACCTGCTG GGTGCCGTCT GTGCGTTCCA GTGAGGCCAA
39501 GGGGTCCTGG CCGGGTTGGG GAGCCCTCCC ATAACCCTGT CTTGGGCTCC
39551 AACCCCTCAA CCTGTATCTC ATAGATGTGA ATCTGGGGGC CAGGCTGGAG
39601 GCAGGGATGG GGACAGGGTG GGTGGCTTAG ACTCTTGATT TTTACTGTAG
39651 GTTCATTTCT GAAAGTAGCT TGTCGGGCTT GGGTGAGGAA GGGGACACAG
39701 GAGCCGTGAC CCCTGAGGAG GCACAGCGCC TTCTGCCACC TCTGGGCACG
39751 GCCTCAAGGT AGTGAGGCTA GGAGGTTTTT TCTGACCAAT AGCTGAGTTC
39801 TTGGGAGAGG AGCAGCTGTG CCTGTGTGAT TCCTTAGTGT CGAGTGGGCT
39851 CTGGGCTGGG GTCGGCCCTG GGCAGGCTTC TCCTGCACCT TTTGTCTGCT
39901 GGGCTGAGGG ACACGAGGGC AACCCTGTGA CAATGCGAGG TAGTGTGCAT
39951 CCGTGAATAG CCCAGTGC GGTTTGCTCA TGGAGCATCC TGAGGCCGTG
40001 CAGCAGGGAG CCCCATGCCC CTGGGTCGTG AGCTTGCCCTG CGTATGGGGT
40051 GGTGTTCATGG AGCCTCATGC CCCTGGGTCG TGAGCTCGCC TGAGTATGGG
40101 GTGGTGTGAT GGAGCCGCAT ACCCTGGGT TGTGAGCTCG CCTGCATATG
40151 CAGGGTCTGT CATGGAACAT CCCAAGTCTG TGCAGCAGG GAGCCCCATG
40201 CCCCTGGGAC ATGAACCCAC CTGCGTGGAA TGCTGTTTGT GAGGTGTCTA
40251 CAGGGTTTAT AGTAGTCTTG TGGACACAGA AATGCACAGG GGACACTTAC
40301 GGACACAGAA ATGCACAGGG GAGGCCGAGC ATAACCAGGG GTGAGGGGCA
40351 GGCAGCAGTT GTAGTTACTG CCGCGGGGCA CTGCTATGTG CAGGGACAGC
40401 CAGCGCCAG CCCATCACCA CTCCCTGGGC TGGCTGGCAG GTATGGCACC
40451 CTGGGAGCCC GGCATATAC CAGGGCACCC CTACGGCTGC CGCCAGTCTC
40501 ATGCCCAGGT GGGTGCTCTG GGCTGGAGCG AGGGCCAGGT TTTGGGCCGA
40551 GGCTTCCCA GGCAATCCTG TGAGCTCCCT TCTAGCCTCT GACCCAGTCT
40601 GGTCTGGCTT GCATGGATGT AGGGCTTGGG GTGGGAAGTT CAGGTCCTGG
40651 CTTTGCCTTT GCCTGATGTG GATGAGCAGC TCACATGCTC AGGGCCACCT
40701 GAGACTGTCA CTGCTCTCCC CTGGCTACTG GGAGGAGTCA CTGAGAGCTT
40751 CGTTACCCCT GCTGCCTTGC CCAGGGCACA CCCTATACCT CCTCATCTGC
40801 TCTTCCCTC CCTGCCCTC TCTGGGCAGG TAGCAGTCCC TGGCCTCTCC
40851 CCCTGGCTGA TCACCTCCC TCAGGCAGTG GAGATCTGCG TCTGGACACC
40901 CTCAGATCCT GTCAATTGCCT GCCCAGAGTC CTTCAGGGGC ACCCCTCTGC
40951 CTTGGTGTGC GGTCCAGGGC TCTCAGCCAG GTGCCGCACC CTCTGGGGTC
41001 TTCTGTCCAG CTCCCTTGCC CCATGTGCTG TCACTGACTC TCCTTGGGAC
41051 TCGCCTGCCT GCTCAGAGCC CTGCAGGGCT TGGTCAGCTG CCTGTTCAGT
41101 GTCAACACTT CCCTGCACAT CTTAAACTG GGCTTTATTT TCGCTGAAGG
41151 AACTGTGTTG GGACCTTGA CATCTGTCAG GTTTGCACAT GCTGTTTTTT
41201 TTTCTCAGCC CACGTGTTCT CCCCCACGTG GGGTAGCAGC AGGACAGACA
41251 GTGAATCACA GAGTCTGCCC TGAGCAGAGG CTGCTGTCCC TGGGACTCCT
41301 AGCCATGGTC AGACTGTACA AAACGGTTTT CCAGAAATGA AATGTAAATC
41351 CATTTTTATA CTGAAAATGT TACTGAAAGT CACTTTTATG AGCATCTGCC
41401 TTAATAAACA GACATTGATT CCCTTATCAG AAGCCTGTCA CACTGTGTTT
41451 CGTTTCATCC TGGGGAGAAC TGCAGATTG GGGTTTCTGG CTGTCATACG
41501 TCACCTGGCT TGCGGCGGAG TGGGAGGCC AGCCTGGTTT AGGGAACAAG
41551 AGTGACGTGA GGAGTAGCAG GGTGCGTCTC CAGTTACCTG AGGGAACAACA
41601 GATATTTTAA GAGATAATAG CATAGCCTAT TTTAATATGT TTTAAAGGCC
41651 ATAAGCATAT CCAGGAAGAT AAATAAACGT GATACAATGT CCACATAGGA
41701 GGAACTTTCT TTCCTGTCAT TGTTTTCTCT CACAGTGGCC TTCAAGTCAC
41751 AGGACGCAGC GATTCCCTGC CCTCTTCGGT GTTATTACAC AGGCAGGACT
41801 TCAGTGTGAC TATCCCTGCC TTCAGTCTTC TTTAGAAATC ACATCTGTGT
41851 TCAATCCATT GTTTAGAGGG AGTGATATTT TCCTGTTCCA CGAAGAGGAC
41901 TTTTGTGTTCA CAATTGGATC ACAATGCAGA GGAGTCTGTT CCTCCCCCGT
41951 CGGCTTCTCG GTGCTGGGAG GGTGACCTGT CCCAGATGAC TCATCACCCCT

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FIGURE 3N

Docket No.: CL001180DIV  
Serial No.: 10/785,106  
Ming-Hui WEI et al.  
Title: ISOLATED HUMAN ENZYME PROTEINS...

42001 GACATGCTCT TGACAAAGGA CACCACCAAG AGGAGATGGC AGCTGTACCG  
42051 GTGCAGCCTC TGTCTGAGGG GGATATTTGC CTCAGTGTGA TTAAAAATCA  
42101 GTCATGAAAG ATTTTGAAT TCAGATTATT TTTATCAGGA ACAGATTTTG  
42151 AACATCCTGA AATCTTTTCC CTGGCATCAT ATTAGGTTT CTTTGTTCAC  
42201 TATGATGTAA AGTTTCAGAC TCTTGATATT TTTAATATCA ACATAGACGG  
42251 TAGGACAAGG AACGGTACCA GAAATGAGTA AAGAGACAAT AATGATAAGA  
42301 TCGATTTATC AAGACATAAC AACCCCAAAT GTATATGCAC TAAATAACAG  
42351 CTTCAAAATA CATGAAGCAA AATGGCAGAA TTGAAGAGAA TGAGATAAAA  
42401 ACAGAAATTTT AACGGGTGCT TTCCGTACTT TGTAAC TGAC AGACATGAGA (SEQ ID NO:3)

**FEATURES:**

Start: 2034  
Exon: 2034-2047  
Intron: 2048-2179  
Exon: 2180-2345  
Intron: 2346-3088  
Exon: 3089-3227  
Intron: 3228-8043  
Exon: 8044-8119  
Intron: 8120-8806  
Exon: 8807-8928  
Intron: 8929-11095  
Exon: 11096-11192  
Intron: 11193-14163  
Exon: 14164-14299  
Intron: 14300-14894  
Exon: 14895-15003  
Intron: 15004-15390  
Exon: 15391-15509  
Intron: 15510-16853  
Exon: 16854-16951  
Intron: 16952-17636  
Exon: 17637-17664  
Intron: 17665-19945  
Exon: 19946-20002  
Intron: 20003-21064  
Exon: 21065-21136  
Intron: 21137-22389  
Exon: 22390-22440  
Intron: 22441-23113  
Exon: 23114-23263  
Intron: 23264-23922  
Exon: 23923-24019  
Intron: 24020-24749  
Exon: 24750-24855  
Intron: 24856-34288  
Exon: 34289-34354  
Intron: 34355-34799  
Exon: 34800-34880  
Intron: 34881-35894  
Exon: 35895-36065  
Intron: 36066-38596  
Exon: 38597-38675  
Intron: 38676-39320  
Exon: 39321-39449  
Stop: 39450

**CHROMOSOME MAP POSITION:**  
Chromosome # 21

FIGURE 30

**ALLELIC VARIANTS (SNPs):**

| DNA      |       |       |                | Protein  |       |       |
|----------|-------|-------|----------------|----------|-------|-------|
| Position | Major | Minor | Domain         | Position | Major | Minor |
| 478      | -     | A     | Beyond ORF(5') |          |       |       |
| 891      | C     | G     | Beyond ORF(5') |          |       |       |
| 948      | -     | C     | Beyond ORF(5') |          |       |       |
| 3311     | A     | T     | Intron         |          |       |       |
| 3616     | T     | C     | Intron         |          |       |       |
| 3910     | G     | A     | Intron         |          |       |       |
| 6028     | G     | A     | Intron         |          |       |       |
| 8299     | G     | A     | Intron         |          |       |       |
| 8373     | C     | G     | Intron         |          |       |       |
| 8424     | A     | G     | Intron         |          |       |       |
| 8680     | A     | G     | Intron         |          |       |       |
| 8700     | C     | G     | Intron         |          |       |       |
| 8996     | A     | C     | Intron         |          |       |       |
| 10590    | T     | C     | Intron         |          |       |       |
| 11090    | G     | C     | Intron         |          |       |       |
| 11710    | G     | A     | Intron         |          |       |       |
| 12591    | G     | A     | Intron         |          |       |       |
| 13431    | -     | T     | Intron         |          |       |       |
| 14746    | C     | G     | Intron         |          |       |       |
| 14975    | G     | C     | Exon           | 277      | P     | P     |
| 16031    | C     | T     | Intron         |          |       |       |
| 16891    | -     | T     | Exon           | 339      |       | V     |
| 19359    | C     | T     | Intron         |          |       |       |
| 19405    | A     | G     | Intron         |          |       |       |
| 19653    | G     | A     | Intron         |          |       |       |
| 19742    | T     | C     | Intron         |          |       |       |
| 20054    | A     | G     | Intron         |          |       |       |
| 20627    | -     | A G   | Intron         |          |       |       |
| 21337    | T     | C     | Intron         |          |       |       |
| 21894    | C     | T     | Intron         |          |       |       |
| 23360    | G     | T     | Intron         |          |       |       |
| 26758    | A     | C     | Intron         |          |       |       |
| 27033    | T     | C     | Intron         |          |       |       |
| 27332    | C     | A     | Intron         |          |       |       |
| 27538    | C     | A     | Intron         |          |       |       |
| 27625    | G     | C     | Intron         |          |       |       |
| 27736    | A     | G     | Intron         |          |       |       |
| 30688    | T     | C     | Intron         |          |       |       |
| 31172    | C     | T     | Intron         |          |       |       |
| 31433    | C     | T     | Intron         |          |       |       |
| 32660    | G     | T     | Intron         |          |       |       |
| 32981    | A     | C     | Intron         |          |       |       |
| 33557    | T     | C     | Intron         |          |       |       |
| 33652    | G     | A     | Intron         |          |       |       |
| 34390    | T     | C     | Intron         |          |       |       |
| 34399    | G     | C     | Intron         |          |       |       |
| 34989    | G     | -     | Intron         |          |       |       |
| 35067    | C     | G     | Intron         |          |       |       |
| 35495    | G     | A     | Intron         |          |       |       |
| 36001    | T     | G     | Exon           | 631      | L     | V     |
| 38948    | C     | T     | Intron         |          |       |       |
| 39160    | T     | C     | Intron         |          |       |       |
| 40405    | G     | A     | Beyond ORF(3') |          |       |       |
| 40794    | C     | T     | Beyond ORF(3') |          |       |       |
| 40961    | A     | G     | Beyond ORF(3') |          |       |       |

**FIGURE 3P**

41891 C T Beyond ORF (3')

Context:

DNA

Position

478

AGGTTTCAGTGTGAGATTCCATCCAGGCTGAAGCCCCCTATCCCTATTCTTCATGTTTCTA  
CATGGAGGAACCTTACCTGGAGAAAACTTCCAGCCTCTTTCTGCTTCCAGAGAAGTAGAG  
TGACTCATTTTGATTGAATTTTCAGAGAACAGATAGGGTGGAGTGTGCTCAGGCTCCTCTGG  
GTACTCTTTCTGGGGTCTGTGGGTGACTGGAGGGGTGTCTTCTGGTGGGCACTCAATTG  
CATAGTGCTTGGTGAGGCAGTTTCATGGCCTAGAGGCTGGGGGATATGTTTGTCTGACTT  
[-,A]

CGGGTGATTTAGTAGCTTGCCCTCTTGCTTGCAGATTTAAGCCTTGTCCTTCAAGCTAGG  
TTTTTAATTTGTGGCAAAGCTGATATTTTGATACCCACCCATCTTATTGCTGTGTCTTTT  
TCATCCGTTTCTGAACTGGGATAGGAAGAGGTGATTATCCTTGATTGTCTAAACCCCGC  
TATTCACCTGTGGGGAAGGTGCCTGTGGGTATTCTTTGTCCACTCTCTCTTCCAACCTTT  
CTCCTCCGGCTTGCTGTGGCTCACCGCCCCCTTCGAAGTAGGCTGGGGGTAGGAATTGAG

891

TGCTCTTTTTCATCCGTTTCTGAACTGGGATAGGAAGAGGTGATTATCCTTGATTGTCTAA  
AACCCCGCTATTCCACTGTGGGGAAGGTGCCTGTGGGTATTCTTTTGTCCACTCTCTCTT  
CCAACCTTCTCCTCCGGCTTGCTGTGGCTCACCGCCCCCTTCGAAGTAGGCTGGGGGTAG  
GAATTGAGGAGTGGGTGCCGAAATGCTCACTAGGCTGGGGCAGTTGTAAGTGGATGTCAG  
GGCTTCTGTGGGCCAGGTGAAGACATGCTGGGGTCTTCTGTGGGTCCCTTGACCTGACTTA  
[C,G]

GGACCACTGGCTGCAGCCTCCAGACGTGAGCCATGTTTCCAACAGTCAGACGCCCCCTGC  
CCTGTTGCGCCCGGCTGTCCCTTCCAAGTTCGGTCACTCGCTCTGCCTCCATCTTCTCT  
TCCCCTGTGCTGCTAAGGCTTTTACCTTTAATTTCTCCTGGGGCCACCCCAACTCCAGC  
GACCCCGTGAGCAGCTGAGGCTCTACCGCGCTCGGTCTTGGCCAGCGACGACGCCCTTCC  
CTGGCGGGGCTCCAGGGCTTCTGGCCCCGTGTGGTCCGCCAGGTGTGGGGGCCACGGCCT

948

TAAACCCCGCTATTCCACTGTGGGGAAGGTGCCTGTGGGTATTCTTTTGTCCACTCTCT  
CTTCCAACCTTTCTCCTCCGGCTTGCTGTGGCTCACCGCCCCCTTCGAAGTAGGCTGGGG  
TAGGAATTGAGGAGTGGGTGCCGAAATGCTCACTAGGCTGGGGCAGTTGTAAGTGGATGT  
CAGGGCTTCTGTGGGCCAGGTGAAGACATGCTGGGGTCTTCTGTGGGTCCCTTGACCTGAC  
TTAGGGACCACTGGCTGCAGCCTCCAGACGTGAGCCATGTTTCCAACAGTCAGACGCCCC  
[-,C]

TGCCCTGTTCGCCCCGGCTGTCCCTTCCAAGTTCGGTCACTCGCTCTGCCTCCATCTTCC  
CTTCCCTCTGCTGCTAAGGCTTTTACCTTTAATTTCTCCTGGGGCCACCCCAACTCC  
AGCGACCCCGTGAGCAGCTGAGGCTCTACCGCGCTCGGTCTTGGCCAGCGACGACGCCCT  
TCCCCTGGCGGGGCTCCAGGGCTTCTGGCCCCGTGTGGTCCGCCAGGTGTGGGGGCCACGG  
CCTCACCGCGCTACCCCACTCCCCCGGCGAAGCTACGCGGCGCTCAGCTTCCAGGGA

3311

TGTATGTGAAGAGGGTTCTCTGGCCGGGCAACAGTCCCGTCAGCTATCTCTTTTCTTTT  
TTTTTCGATCTCTTTGCAGAAGAATTACTTTAAGGACTTGCCCAAAGCCACACCGCCTTT  
GAGGGGGCTCTGAACGGGATGACATTTTACGTGGGGCTGCAGGCTGAGGATGGGCCTGG  
ACGGGTGATTATGGTGGCCACTTTTCTCTCTGCCAGGTAGGAGTATGCTGCCCCAGCCT  
GATGGTATGGCCACCCTGGATCACCTTGGGATCCTGGCCAGCCTGGTCTAGGGTTTGT  
[A,T]

TGAAGCAGGTGAAAATCCAGGGGCTCACAAGAAAAGGGCTGGCAAACCTCTGCCCTATGTC  
AGAGTCGTCTGCTATTGGTCTAGGGGATCAGCTAGCCTTGCCAGTGTAGGGTGACAGGC  
TCTCTGATAAGAGAAGCAAGTGGTTCTCTAGGGCTCTGTGTTGCCCTTGAGGGAGGAGGAA  
GGTGGGCTTTGAAGTCTCAGTACAGGATGGGATGGACATTCCAGGTGGAAGGCCACGCT  
ATGCCAAGGGGCTGTAGGTGGGCAGAGTGGTGGGTGGGGAGCTGATATCTGCTGTGAACT

3616

GCAGGTGAAAATCCAGGGGCTCACAAGAAAAGGGCTGGCAAACCTCTGCCCTATGTCAGAG  
TCGTCTGCTATTGGTCTAGGGGATCAGCTAGCCTTGCCAGTGTAGGGTGACAGGCTCTC  
TGATAAGAGAAGCAAGTGGTTCTCTAGGGCTCTGTGTTGCCCTTGAGGGAGGAGGAAGGTG  
GGCTTTGAAGTCTCAGTACAGGATGGGATGGACATTCCAGGTGGAAGGCCACGCTATGC  
CAAGGGGCTGTAGGTGGGCAGAGTGGTGGGTGGGGAGCTGATATCTGCTGTGAACTTCTC  
[T,C]

FIGURE 3Q



GGGGCTATTGCAGGAGAGCTTCAGGTTTCAGGCTGGTGAGTAGGAGGAGCATAGCAGTTGG  
ACTGCCTGGGTATTGAACTGATTGGCTACACAAGACTATTTTGCATCCTGGGAGTGT  
CTCTACAGAAATCCTCAGCCTTGTAATAATGGGAAATTCCTCCTATGAATTTATGCAATA  
GGACTTTTTTCCCTAGTGACTTGTAATCACATTGTTTCAATGACGTGAATTCCTACATAA  
ATAGGTTTTGTTTCTGTGATAACTCTTACTGATACATCATTTTCTTTTACTACGCTGACT

3910 CTTCCTCGGGGCTATTGCAGGAGAGCTTCAGGTTTCAGGCTGGTGAGTAGGAGGAGCATAG  
CAGTTGGACTGCCTGGGTATTGAACTGATTGGCTACACAAGACTATTTTGCATCCTGGG  
AGTGTCTCTACAGAAATCCTCAGCCTTGTAATAATGGGAAATTCCTCCTATGAATTTA  
TGCAATAGGACTTTTTTCCCTAGTGACTTGTAATCACATTGTTTCAATGACGTGAATTC  
TACATAAATAGGTTTTGTTTCTGTGATAACTCTTACTGATACATCATTTTCTTTTACTAC  
[G, A]  
CTGACTTTGTAATAGATAGAAAGTCCCTTATATACCTTTGTTGCCTTTCTTTTTAAAAACAT  
CTCTTACCTGTGTCTATTCACTTACTCATCCAAATGCCTTTATCCTGATTTTGTCCCAG  
ACTTGAAATGAAGTTGCAATAGGCTTATATGTTAGTTTGGGAAGAGTTGGCCTTTAACGT  
TAAAAACAGTTCCATGGTGTCTTACTGTAGGCCAAGCCCTGCTCAAGGCCTGTTCTCTTT  
TAGTCCCTAGAATAAGCCTAATGAGATACATTAGAAAGCTGAGGCACATTTATCCAGGT

6028 GTCTCTTGCCCTTGCCACCAAGGTGGCTTGCCACCCACAGCCTCTCGAGTAGCTGGGATTA  
CAGCCATGTGCCACCATGCCTGGCTAATTTTTGTATTTTGGTAGAGACAGGTTTTCACC  
TTGTTGGTCAGGCTGGTCTCGAACTCCTGACCTCGTGATCCCCACCCCCACCCCCAGC  
CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCACCTGGCTGAGTTGGAGCTTTTC  
TTCCCTCTTTTTGGACTTTGGAATAATGCTCTTGGTCCATGATGCTATGTAGACAGCTCCC  
[G, A]  
TTGACTGTGGCTGTGCGGCATTGGGCAGCACTCTGGTGAACACTGAATCGGGTCTGACC  
TCCTAGCCCCACCATTTACTGGCTGAGCCTCAGTTTCCTTGCCGTGTAATAATCAGGAAGAT  
GCTGGCTCTGCTCCTCTCTGCACATTTCCCCGCTCCTAACAACATTATAACTGTTAGGAAA  
GAGACGGGCTTGTTTGGGATGGCTCATTTTATGTGACCCCTGTGCGCTGTCTCTGAGTCC  
ATCTGCCCTTCTTCCAGGGTGTAGGGACCAGCCCCACAGGGTCGGTGGGTCTCTCCCTGT

8299 CATGACCACCTGTCCCCAGTGAGGAACATCTCTCTGCCACACAGGCCTCCTGATCACTT  
GCCACGTGGCAGCATCCCTCTGCCAGCCGGATACAGAGAAGAGATTGTGCGGTACCTGC  
GGTCAGTGACGCTCCCTGACGGTGGCTGGGGCCTGTGAGTGTGCCTGCCCCGTGTGCTACT  
GCACATGTGCATGTGTGTCTCATGATGTAGGAGATGCTTGGGTTCAGGCAGCTGC  
CAGGGGTAGGAGTGATTGCAGCTGTGGGTGTGGGTGAGGGAGAGACTAGCAGGC  
[G, A]  
GGGAGTGGGCTGAAGGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTAAATGGAT  
TTTGTGGCTGTACGACACTCTTGAGACCCACATGTGAAAACGTGCTGCTGTTATCACT  
TAAGACAGAAGAAAATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGAC  
AGCTTTCTGCCATGTGGCACACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCC  
CTTGAGCTAGAAGTGTGACTCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAG

8373 ATCCCTCTGCCAGCCGGATACAGAGAAGAGATTGTGCGGTACCTGCGGTGAGTGACGCTC  
CCTGACGGTGGCTGGGGCCTGTGAGTGTGCCGCCCCCTGTGCTACTGCACATGTGCATGT  
GTGTGTTCTCATGATGTAGGAGATGCTTGGGTTTCCAGGCAGCTGCCAGGGGTAGGAGT  
GATTGCAGCTGTGGGTGTGGGTGGGTGAGGGAGAGACTAGCAGCGGGGAGTGGGCTGA  
AGGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTAAATGGATTTTGTGGCTGTTA  
[C, G]  
GACACTCTTGAGACCCACATGTGAAAACGTGCTGCTGTTATCACTTAAGACAGAAGAAA  
ATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTTTCTGCCAT  
GTGGCACACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGAGCTAGAAGT  
GTTGACTCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAGGAAGGAGTGGGGG  
CTCAGTTGTATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAGGGGTCTCCT

8424 GTGCAGCTCCCTGACGGTGGCTGGGGCCTGTGAGTGTGCCTGCCCTGTGTCACTGCACA  
TGTGCATGTGTGTGTTCTCATGATGTAGGAGATGCTTGGGTTTCCAGGCAGCTGCCAGGG  
GTTAGGAGTGATTGCAGCTGTGGGTGTGGGTGGGTGAGGGAGAGACTAGCAGCGGGGA  
GTGGGCTGAAGCCATGCAGGTGGGGCCTCGGCTTCACATCTTTTGTAAATGGATTTTG  
TGGCTGTTACGACACTCTTGAGACCCACATGTGAAAACGTGCTGCTGTTATCACTTAAG  
[A, G]

FIGURE 3R

CAGAAGAAAATTGCCCTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTT  
TCCTGCCATGTGGCACACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGA  
GCTAGAAGTGTGACTCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAGGAAGG  
AGTGGGGGGCTCAGTTGTTCATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAG  
GGGTCTCCTGTGTTGACATGTTATGTCAGGTTAAGCCATTTTAGCATTCTTAGTTTCTG

8680 CTTGAGACCCACATGTGAAAACGTGTCAGTCTGTTATCACTTAAGACAGAAGAAAATTGCC  
CTTGACTCTGGGCTGGCAGCAGGTGGAGACAAGGCCTGACAGCTTTCCTGCCATGTGGCA  
CACACTTTGGGAGCAGAGCCATAGCCCAAAGTGGACCGCCCTTGAAGCTAGAAGTGTGAC  
TCAGGCGTGGGAAGGTGTAGAGCAGGCGGGTCACGGTGAGGAAGGAGTGGGGGGCTCAGT  
TGTCATGGGAGGTGCATGAATTCGTACTGCAGAGTGGCTGCTCAGGGGTCTCCTGTGTTG  
[A, G]  
CATGTTATGTCAGGTTAAGCCATTTTAGCATTCTTAGTTTCTGAGGAAACTCCACAGAA  
AGTTTTGCTTTATTTCTTAGAAGTAAGGACAGATACCGGTTTCTCACCTGTCTCTGCTC  
CTGTAGGCACATTGAGGATAAGTCCACCGTGTGTTGGGACTGCGCTCAACTATGTGTCTCT  
CAGAATTCTGGGTGTTGGGCCGTGACGATCCTGACCTGGTACGAGCCCGGAACATTCTTCA  
CAAGAAAGGTACGGCATGTGCAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAAT

8700 ACTGTCAGTCTGTTATCACTTAAGACAGAAGAAAATTGCCCTTGACTCTGGGCTGGCAGC  
AGGTGGAGACAAGGCCTGACAGCTTTCCTGCCATGTGGCACACACTTTGGGAGCAGAGCC  
ATAGCCCAAAGTGGACCGCCCTTGAAGCTAGAAGTGTGACTCAGGCGTGGGAAGGTGTAG  
AGCAGGCGGGTACGGTGAGGAAGGAGTGGGGGGCTCAGTTGTTCATGGGAGGTGCATGAA  
TTCGTACTGCAGAGTGGCTGCTCAGGGGTCTCCTGTGTTGACATGTTATGTCAGGTTAAG  
[C, G]  
CATTTTAGCATTCTTAGTTTCTGAGGAAACTCCACAGAAAGTTTTGCTTTATTTCTTAG  
AAGTAAGGACAGATACCGGTTTCTCACCTGTCTCTGCTCCTGTAGGCACATTGAGGATA  
AGTCCACCGTGTGTTGGGACTGCGCTCAACTATGTGTCTCTCAGAATTCTGGGTGTGGGC  
CTGACGATCCTGACCTGGTACGAGCCCGGAACATTCTTACAAGAAAGGTACGGCATGTG  
CAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAATGAGCTCTCACAAACGAGATA

8996 TAAGCCATTTTAGCATTCTTAGTTTCTGAGGAAACTCCACAGAAAGTTTTGCTTTATTT  
CTTAGAAGTAAGGACAGATACCGGTTTCTCACCTGTCTCTGCTCCTGTAGGCACATTGA  
GGATAAGTCCACCGTGTGTTGGGACTGCGCTCAACTATGTGTCTCTCAGAATTCTGGGTGT  
TGGGCCTGACGATCCTGACCTGGTACGAGCCCGGAACATTCTTACAAGAAAGGTACGGC  
ATGTGCAGCATGTGCTGGGCCAGGGGTTCGTGTCAACTCGATAATGAGCTCTCACAAACG  
[A, C]  
GATACAGAAAGATGCACTTGCAGCTGAAACAGTGGGCAAAAGCACATGAGCAGGGAATTT  
GTCAAAGCAGAAGTAGGCAGACACTGTTTAACCTAGGCATCATTTTAAAAAAGCAAAT  
TAAGAGCCAGGCACAGTGAGTGGCTCACGCCCTGCAATTCAGCAGCTTTGGGAGACTGAGG  
TAGAAGGACCCTTCAACCTAAGAGTTCGAGGCCAGCCTGGGCAACATAGTGAGACCTGG  
TCTCTACAAAAACAATAAAATATTAGCCAGGTGTGATGATATGCACCTGTAGTCTCAGCT

10590 CATGAGATCCTGCCTTCTTTCTTGGTGAGCTTGTCATATTGTCCTCAGTTCACTGTCAG  
CCTTTGGTGTGCTGATGCTGCGTCCCCAAGGCTGCTGTCCGGTTCCCACCACACTCCTG  
GCGCTTGCTTGGTGAAGGAACGTGTTAGGCTGCACCTTGCCCTAGTAGCTTTGTGGGTCT  
TTATTGACTTTTGCATACCTTTTGGGGTTTGGAGCAGGGACTCCTCAGAAGCATGTTTAG  
ATGGTGTGGCTGTGCCAGGACTGCTGCTGCTGAAGTGGCTCTGGCATGGGGCCAGCGTGC  
[T, C]  
GGAGCTACTCTGGAGTCTAGGGTCGTCTTTGTTCCCATACAGGACCAGTCTGCCAAGTGG  
AGATGACACAGACTGGGGCAGCTCAGGCTTGGCTCAGAGGGCGAGGCTGAGTGTGCGCTG  
TCACTTCCCCACCTTGCCCTTCCAGGCGCATGTGCACCTGGGCCCTCGCTCACCTGAG  
CACTGAGGTGCTCCTGGACCTTCCAGGTAGCTGTCTTATGCTGCTCCTTCCCTGGGGCCA  
GGGGTTGCAAAACACCTCTCCTGGGGCTGGACACACACACTCCCAGGAAAGCCACTGGTTT

11090 CTCCCAGGTAGCTGTCTTCATGTGCTCCTTCCCTGGGGCCAGGGGTTGCAAAACACCTCTC  
CTGGGGCTGGACACACACACTCCCAGGAAAGCCACTGGTTCCACCTAGGGGGCCGTGTAT  
CCAGGCAAGTTCTCAGCACTCTGGAACCTGCTTCGCACATGGGGGTGCAAGATCCACAT  
GAGGCTGCCCTTGCCCTCATGGAGAGGGGCACACGTGACTCCCAGAGGGTGAAGCTTCCCA  
GCTAGAGGCAGTGCAGACTTTGCTGACAGGAAGCAGATGACGTGGGCCATTCTCTCCCC  
[G, C]

FIGURE 3S

14975 CTGGGCAGACCTGGGACTCATGGAGCTGGGGAGCTCCTCAGAGCGGTCTCCCATAGGGG  
GCCTTCATGTGCCCTCGGGGTCAAGTTGCTGGAGGGACCCCCACCCAGGAAGGGACTGGCC  
CAGGGCCCTGAGGGCGGATGGTGGGAGGCCACCCTCCTGGTTTGAGCCAGGCCACCAG  
GTGCTCCCAGGCCCAAGGCTCAGACACTGCCCTACCAGGAGCTCTATGTGGAGGACTT  
CGCCAGCATTGACTGGCTGGCGCAGAGGAACAACGTGGCCCCCGACGAGCTGTACACGC  
[G, C]

FIGURE 3T

CACAGCTGGCTGCTCCGCGTGGTATATGGTGAGCGCCTCCTGAGGGGCCGGCAGGGCAGC  
CCAGGGTCAGGGTCAGGGTGTGCGCCACTCATTCACGCACTCATCCCCTGCCAGCGGCAC  
TGGGCCACCTCCTCTGTGCCAGGCCCCAGGGGGCGGGATCTCATCGCCCTGCCCTCCAC  
CCTGAGAACCAGCTGGTCTTCTACTCTCAGGAGTCCACCCTGTGCAAGGGTGTGTGGTAG  
GAGGTGTGGGGCAGCCCCCTCTGGGCAGGGAAGGAGGAGCTCAGAGACCAGGCCTGGGGG

16031 TTCCGTCCCCACCGGCTCTTGTCCTCAGTGTGCCTGGACACTCTCCTAGAGGCCCTCC  
CTGAGATCTTGTGGCTAGCTGGCTAGCTGGGAGGGGTGCTTTTTCCTCACTTGGTTCCC  
TCTCCCCAAACAGTTCATCATTCGCCATTCTCCCGTGGGGTTTAGACATGCCAGGGTGG  
GTGGGAGTAGCAGGTGCCACTCCTGATTCTCTCCTGCTAGCTAGGAGCTTGGAGCTCTCA  
CCTCTGTGGGGCCTGCAGGGGTCCAGGTGTGGCCAGTTTCACTGACCTTAGAGGGTGAAT  
[C, T]  
CCCGGGCTGTGCTGGTGGCGTGGCCGCTCCTGACAGAGTCAGCAGGCCCTGGGCTGTGCT  
GCAGCTGTGCGGTAGCTGTGCGGTAGCTGTGCGGTGTAGTGGGTGGCTTAGGCATT  
CTCTGGACATACCAGGTGGCACTGGGCCACTGAGTCCCACCCTGACACTGCATCTCGGA  
TTTCTTGGGCCCTCATGCCACCTCAGTGGATCACAAATCCTGACTGACCCTGCAGCGGGTC  
CCTGTGTTTTTGTCTCAGCAGTGATGTGGTCTTTGTGGGTTTTGGTTTAATCCCATATAG

16891 GTGGAGTGTGCTCCTTCTCACAGCCTAAGGCAGGCTGTGGCCTTGCCGACACTGCCTC  
TGCTGAGTTGGGTCTGGGGACACAGTTGTTGCCCATCCTCGCTCAGGAAATGCCTGTT  
AGAGCAGAAGGCCCTGTCTGGCCCTGAGTGATCTGCACGGCACTTTATGCCTGGGGGC  
TGCTGTGGATCTGGACGAGACCTTGTCCCTGGAGGCTGTGTGGGTCTGGAGCGGAGCCT  
TGACAGGGCTGTCTCTCCTGCAGATCTCGAAAACCATCAACATGCTTGTGCGCTGGTATG  
[-, T]  
GGACGGGCCCGCTCCACTGCCTTCCAGGAGCATGTCTCCAGAATCCCGGACTATCTCTG  
GTGAGTGTGGCTGGGATATGCTGGCGGGGCTCTCACGAAGACTGGATCTGAGCCCCAGC  
TGATCCCAGTGAGGGGGCCCCACGGTGCCATCTGGGAATACTGCCAGGGAATACCTCC  
AGGAACCAGCAGTGTGAGGGCTTGTGGAAGCCACTGAGGGTTGTCTTGAATTGGAAGAT  
TTGCCACCCAGTGAAGTGTGGGTGTTCCCAGAAGGTAGAGTGAGGAAGGGGTGGTAG

19359 CCACACACCACCCCTGCCAGTCCCCATGTCTGTCTGGTCAGTGCCCAGCTCTGTCTCA  
CTAGGGTTTTGGTCACCGGCCCTTTGAACTGAGACCAGGCTGTGTACCTGTGAGCCAGCT  
CGGGGTGAGATTTGAGGTGGAGCCTTCCAGCCCTGTGCAGAATTCCCATCACCTCCAGG  
TGTAATCCCTACACTTTGGGAGGCCAAGGTGGGCGGATCACAAGGTCAGGAGATAGAGACCATCCTGGCTAACA  
[C, T]  
GGTGAAACCCCGATGCTACTAAAAAATACAAAAAATTAGCTGGATGTGCTGGCAGGAG  
CCTGTAATCCAGCTACTCCGGAGGCTGAGGCAGGAGAATGGCGTGAACCCAGGAGCGG  
AGCTTGCAGCGAGCTGAGATCACGCCACTGCACCTCCAGCCTGGGCAACAGAGCGAGACTT  
CATCTCAAAAAAAGAAATGGGGTCAATTTCCAGGCATCACCATGACTGAGGTGCGCCA  
CTGTCAATTGGGTGAGAGCAGCTGGATGCTCTATGTGTAGGTGCTGGAGCCTCTGAGGGAT

19405 CCAGCTCTGTCTCACTAGGGTTTTGGTCACCGGCCCTTTGAACTGAGACCAGGCTGTGTAC  
CTGTGAGCCCAGCTCGGGGTGAGATTTGAGGTGGAGCCTTCCAGCCCTGTGCAGAATTC  
CCATCACCTCCAGGTGTACTCAGAAATGGGGATCATTTGGCCAGGTGCGGTGGCTCACGCC  
TGTAATCCCTACACTTTGGGAGGCCAAGGTGGGCGGATCACAAGGTCAGGAGATAGAGAC  
CATCCTGGCTAACACGGTGAAACCCCGATGCTACTAAAAAATACAAAAAATTAGCTGG  
[A, G]  
TGTGCTGGCAGGAGCCTGTAATCCAGCTACTCCGGAGGCTGAGGCAGGAGAATGGCGTG  
AACCCAGGAGGCGGAGCTTGCAGCGAGCTGAGATCACGCCACTGCACCTCCAGCCTGGGCA  
ACAGAGCGAGACTTCATCTCAAAAAAAGAAATGGGGTCAATTTCCAGGCATCACCATG  
ACTGAGGTGCGCCACTGTCTATTGGGTGAGAGCAGCTGGATGCTCTATGTGTAGGTGCTGG  
AGCCTCTGAGGGATCGTCCAGTCTAGAAAGTGTCTCAGAGGGACACTGTCTGCCTGGT

19653 CTAACACGGTGAAACCCCGATGCTACTAAAAAATACAAAAAATTAGCTGGATGTGCTG  
GCAGGAGCCTGTAATCCAGCTACTCCGGAGGCTGAGGCAGGAGAATGGCGTGAACCCAG  
GAGGCGGAGCTTGCAGCGAGCTGAGATCACGCCACTGCACCTCCAGCCTGGGCAACAGAGC  
GAGACTTCATCTCAAAAAAAGAAATGGGGTCAATTTCCAGGCATCACCATGACTGAGG  
TGCGCCACTGTCTATTGGGTGAGAGCAGCTGGATGCTCTATGTGTAGGTGCTGGAGCCTCT  
[G, A]

FIGURE 3U

AGGGATCGTCCAGTCCCTAGAAAGTGTCTCAGAGGGACACTGTCTGCCTGGTGGCCCATG  
AAGAAAGGGAGGGCTCCCTGAGTCTCCCTGACGTGTGTCTGCCTGCAGGGCTCAGCCTTC  
TCTGAGGCCCTTGTGAGCCATGAGGGGTGCCAGGGCTCAGAGCCTGAGGCTGAGCGTTG  
GCTGGGTGGGAGCCCCACACCTGGCCCTCAGGCGCCATTGGATCCTGGAGGCAGTGGC  
TGGGAGTGGGAGGGGCTGCATCTGCTGTCTGTAACACCATCCTTTGTGTGTAGGGCACCA

19742 AGGCTGAGGCAGGAGAATGGCGTGAACCCAGGAGGCGGAGCTTGCAGCGAGCTGAGATCA  
CGCCACTGCACCTCCAGCCTGGGCAACAGAGCGAGACTTCATCTCAAAAAAAAAAGAAATG  
GGGTCATTTCCAGGCATCACCATGACTGAGGTGCGCCACTGTCAATGGGTGAGAGCAGCT  
GGATGCTCTATGTGTAGGTGCTGGAGCCTCTGAGGGATCGTCCAGTCCCTAGAAAGTGTCTC  
CAGAGGGACACTGTCTGCCTGGTGGCCCATGAAGAAAGGGAGGGCTCCCTGAGTCTCCC  
[T, C]  
GACGTGTGTCTGCCTGCAGGGCTCAGCCTTCTCTGAGGCCCTTGTGAGCCATGAGGGGTG  
CCCAGGGCTCAGAGCCTGAGGCTGAGCGTTGGCTGGGTGGGAGCCCCACACCTGGCCCT  
CAGGCGCCCATTTGATCCTGGAGGCAGTGGCTGGGAGTGGGAGGGGCTGCATCTGCTGTCT  
GTACACCATCCTTTGTGTGTAGGGCACCAACGGCTCACAGATCTGGGACACCGCATTCG  
CCATCCAGGCTCTGCTTGAAGTTCTGGCTCCTTCTCTTTTCTCAGCCTCAGCTGACCTT

20054 GCCTGCAGGGCTCAGCCTTCTCTGAGGCCCTTGTGAGCCATGAGGGGTGCCAGGGCTCA  
GAGCCTGAGGCTGAGCGTTGGCTGGGTGGGAGCCCCACACCTGGCCCTCAGGCGCCCAT  
TGGATCCTGGAGGCAGTGGCTGGGAGTGGGAGGGGCTGCATCTGCTGTCTGTAACACCATC  
CTTTGTGTGTAGGGCACCAACGGCTCACAGATCTGGGACACCGCATTCGCCATCCAGGCT  
CTGCTTGAAGTTCTGGCTCCTTCTCTTTTCTCAGCCTCAGCTGACCTTCTGTGACGT  
[A, G]  
AGCCACGCATCCACCTGAGGGCAGCACTGCTGGCCACACACTTGCCACTCCTCGATACT  
TCCAGTGACCTGGGCTCTGGCCTTGGCTTTCAGAGGGTCTGTGCTGTGGAGGGGGCGCCT  
TGGCCAGCAGCCTTGGGTGTTGGGCTGGGTGGGGGCTTGGGAGGGCAGGGGCTGGAGG  
CTGTGTGAGAAGGGAGTCTGGTGAAGGCTGTTTCTGAGAGTGCAGGCAGGAGTGGGACT  
CCAGGCTCTTCTTAGAACTGGAATGCTTGGGCCAGGCACGGTGGCTCACACCTGTAATC

20627 CCAGGCACGGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCGAGGAGGGTGGATC  
ACGAGGTGAGGAGTTCAAGACCAGCTGGCCAAGATGGTGAAACCCGTCTCTACTAAAA  
GTACACAAAAATTAGCCAAGCGTGGTGGCGGGACCTGTAATCCAGCTACTTGGGAGGC  
TGAGGCAGAGAATTGCTTGAACCCGGAAGTGGAGGGTGCAGCGAGCCGAGATTGTGCCA  
CTGCACTCCAGCCTGGGTGACAGAGAGAGGCTCCGTCTCAAAAAAAAAAAAAAAAAAAAA  
[-, A, G]  
AACTGGAATGTTTGTATGGGCATTCTCGAGCCAGTACTGGAGAAAAACGAGAGTGGAT  
TTTTATGCCGGTGGGAATGAGGTAGGTGGGATTCTGAAGGTGTTTCTGGAGAGCCCTGAG  
GGCTGGGGCCACGCAAGGGGCTGCCTACACAGGGTCTGGAGACCCCTCTGGGCATGGATG  
CTGGCCAGGCAGGGGGTGTGGCATCCATAAATGGTCTCCTGCGCCCTTCCATCTTCAG  
TCATATCTCATGGACTTTTGTGTTTGTCTTTAAAGGTAAGTGCAGCAGGAGACCTTGG

21337 AGCCTCTCTGTCTGTCTCTTCCAGGCGGGCGGGACACAGGCCGAGTTTTCGTC  
CTGCCTGCAGAAGGCTCATGAGTTCTGAGGCTCTCACAGGTGAGGCCGGTGCCTGGGGC  
TCTGAGGGGGCTGAAGAGGGGATCAGGGCTGGGAGCTCCTGCAGGCAGAAAGTGCACC  
TCACCTCCACCTGCCCCATTTCTGCACTGGTGTTCAGGGTCACCCCCACCTCCCAT  
CCCCCTCCCTAGCCCCGTCTCCATCCACCGGTCTCCTCGGGCTGGCCTCACCTGGGGCAG  
[T, C]  
TCTCTGAGGCCTGCAGGGTGTGGGGGTGTGGCAGTTTCTGCGTCTGTCTCATGTTGGA  
GCCACTGTGTGCAAGGGCCAGGCACGGGCAGGGGCTGTGTACCTGAGCTGCACAGCCTA  
CACGGCACCTCCATGTCTCTGAAGCACCTTCTGCCATGAGAGGTGACGCCAGCCTGTGGA  
CTTGCCCTCCTGAGACTGTTTGCAGCAAAAGCCCCGGTCCCTCCTGCCAGATCAGCTGCC  
CACAGACCCTGCCCCGAGCCATAGTTTGACCTCAGTGTCTCTCACAGTGCCTGCACCCC

21894 GCCCATAGTTTGACCTCAGTGTCTCTCACACGTGCCTGCACCCCAGTCTGCAGCCACAGT  
CATCCCATACATGCGCCCCAACCTCCCGTGTCTCCACACCCGTGTCGGGCCACGGCCTC  
AGCCAGTGTCCTCTGCCTGGAACCGCTGCCCCCAGCCCCGTCTCCCTCCCTTCAGCTC  
TCATAGGACATTGTTCTGAGGGCTTCTGGGTCTTCTGGCCTCTGTGTGGCCAAGGCT  
GGCACCCATCTTGGGCTCAAGCAGAGGAGGGGCATTGTCCTGTGTGCTGGCCCAATGG  
[C, T]

FIGURE 3V

GGCCTGCTCCTGCTCCTGCCTCCTGCCCAGGACTTGCTCTGGGTGATGGGGACTTGGGGA  
GGCTGACTGAACCTTACGGCACTCCAGGCCTCTTCCCTTCTCAGTGGGTGAGAGAGGCA  
GCCAGAAGCTGAGGTTGTTTACAGGAGCATTTGGGGGCGCCTGGCACAGAGCACACCCGAG  
AGACCTGGGCCCCCTCCCTGCCTTCTGGCCGGTGGGGAGATCACAGGGGAGTCAGGTGCT  
GACTCCCAGTCCCGTCTGGGCTGGTTTGAGCCCTCGCTGGCCAGTCACGTTTCCACAGCAG

23360 TGAGAACTGGGGTGTGGACACCCCCAGCCTGGAGTCATGGCTTGTGCTCTGCAGGGTGGC  
TTCTCCTTACGTACGCTGGACTGCGGCTGGATCGTTTCTGACTGCACGGCTGAGGCCCTTG  
AAGGCTGTGCTGCTCCTGCAGGAGAAGTGTCCCATGTACCGAGCACATCCCCAGAGAA  
CGGCTCTGCGATGCTGTGGCTGTGGTAAGGCTGTGGTCCCAGCAGCCCCGTCCATACCTC  
GTGTCCTGCAGATGAGCTGCGTGCTCACTTCCACTCCTGTGGGCTCCAGCCCAGCACACA  
[G, T]  
TCCGCGCAGGCCGTAGGAGCTTGTCTTGGATGGTGTCTATATGTGGAGAAGTGTGAGCT  
CTGGCTGGACCCCTAGGGGCCCTTGTCTGGGCTGTGTGCACAGGGCCCTGCACGTGGGAGCT  
GGTGTCCAGCCCAGCCACCGATACTTGGGGGAGCCGGCGTGGCCCCAAGGTTTCTCTCT  
GGTGGTTTCCACTGGGTGTCTGAAGAGGGAATTTGTGGTGTGGTTTGGTGCCACATC  
CTTTCAGCACATCTGGCTTTTGTGTGTGTTCAGTGGAGACCCTGCCCTTTCTCGGA

26758 CAACCTCCGTTTCCGGGGTTCAAGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGAC  
TACAGGTGCTGACCACCATGACTGGCCAATTTTTTGGTATTTTTATTAGAGACAGGGTTT  
TACCATGTTGTCCAAGCTGGTCTTGAACCTCCTGACCTCAGGTGATCCACCTTCCCTGGCC  
TCCCAGAGTGCTGGGATTACAGGTGTGAGCCACCACACTGGCCTTGTCTATTTCTTTCT  
CCTTTATTTTTCTAACTTGAATACCTTAGATATTTGATTTTTCAGGCTTTTATTGAAATATG  
[A, C]  
ATTTGAGGCTATAAATGAGTTTGTAGATATCATTCAGTTAAATGTGTGTTCTGGTGCTTG  
CTGTGGTAGCACAGATACTAAAAGTGTCTTCTGTCTTCTACTGTTCTCTCTGGCCCATGA  
GTTATGTGGGAGTATGCTGCTTCAATTTACAATCTGAGAATGTTCTGGTGTGGTTTTTTTG  
GAAGCCGTGGATGGAGCAGGGGTTTTCTTGTGCTTACAGGTGCAGCTAGGAGGGCACTG  
TGTCAGGGTCTTCTGTGCGCCTGGCGTGGCCCTTGGCCATGTGTGCTCTGCGGCATGA

27033 ATTTTCAGGCTTTTATTGAAATATGAATTTGAGGCTATAAATGAGTTTGTAGATATCATT  
CAGTTAAATGTGTGTTCTGGTGTCTGCTGTGGTAGCACAGATACTAAAAGTGTCTTCTGT  
TTCTACTGTTCTTCTCTGGCCCATGAGTTATGTGGGAGTATGCTGCTTCAATTTACAATCT  
GAGAATGTTCTGGTGTGGTTTTTTTGAAGCCGTGGATGGAGCAGGGGTTTTCTTGTGCT  
TCACAGGTGCAGCTAGGAGGGCACTGTGTCCAGGGTCTTCTGTGCGCCTGGCGTGGCCCT  
[T, C]  
GGCCATGTGCTGCTCTGCGGCATGAGGTGGGCGTGAGTTGTCTCAGCCACATTTAGAGA  
ATTGGCCTTTTAAAAATAGATCATCTTTTAAAAATCACTGTAATAAAAGTAAAGCAGGT  
TCTTTGCAAAACAAGACTTGCAAAATACAGAGAAGCGCAAAGAAGAAGCTAAGTCGCCCCCT  
CCTCGCCCCCTGAAGGAGAATCTGCTGTTGCTGTTTGGTCTCCACATTTCCATGGCGGCTT  
GCTGCCCTTTTACGCCTGGCCCACTTTGTGCCTGGTGAGGTTTCTAAAAGCCCCACCT

27332 TTGGCCATGTGCTGCTCTGCGGCATGAGGTGGGCGTGAGTTGTCTCAGCCACATTTAGA  
GAATTGGCCTTTTAAAAATAGATCATCTTTTAAAAATCACTGTAATAAAAGTAAAGCAG  
GTTCTTTGCAAAACAAGACTTGCAAAATACAGAGAAGCGCAAAGAAGAAGCTAAGTCGCCCC  
CTCCTCGCCCCCTGAAGGAGAATCTGCTGTTGCTGTTTGGTCTCCACATTTCCATGGCGGC  
TTGTGCCCCCTTTACGCCTGGCCCACTTTGTGCCTGGTGAGGTTTCTAAAAGCCCCACC  
[C, A]  
TTGAGCGCGCTCCTCCAGCACGAGCAGTAATGGCACAGGTGTTGTGTCATTTTACTCAGT  
AGCCTCTGGGTTATTTTTTCACTTTTCCCTGTTGTTTTTTAGCTTTTCCCCATTTTAACTT  
TAACCTGATTTTCTTGTAAATATTTATTCATGACCATTATTATCCCTAGAGCCACAT  
GGCTTGGGGTCCACCTGCCTGGGTCGCCCCCATCCCTGCCCCCTTGGCTGTCTGACCT  
GGCTTGGTGACTTCTCTTCTCTCATCTCTCTCCCTGCCTGAGTGGGCAAGAGTACAG

27538 GTGTGCTGTTTGGTCTCCACATTTCCATGGCGGCTTGCTGCCCCCTTACGCCTGGCCCCA  
CTTTGTGCTGGTGGGTTTTCTAAAAGCCCCACCTTGAGCGCGCTCCTCCAGCACGAGC  
AGTAATGGCACAGGTGTTGTGTCAATTTACTCAGTAGCCTCTGGGTATTTTTTCACTTTT  
CCTTGTGTTTTTTAGCTTTTCCCCATTTTAACTTAACTGGTATTTTCTTGTAAATAT  
TTATTCATGACCATATTATTCCCTAGAGCCACATGGCTTGGGGTCCACCTGCCCTGGGCT  
[C, A]

FIGURE 3W

GCCCCATCCCTGCCCCCTTCTGGCTGTCTGACCTGGCCTGGTGACTTCTCTTCTCTGCTC  
ATCTCTCTCCCTGCCTGAGTGGGCAAGAGTACAGCCTCACAGAGTGGTGGGATTGTGTGA  
GATGCCACAGGGAAGCACATGTCAGTTGTTGTCACTGTGTAGAACAATGAGTCCCGGATG  
TGGCCCGCAGGGGAGCAATGGTGACTTAATCGCGGGCTTCCTCTGCATTTCCTTTGGTGAC  
TTCCAAGCTAGAACATTCTTTTTTGTGTTATTGTTTGAAGCAGGGTCTCACTCTGTTAC

27625 CCCCACCCCTTGAGCGCGCTCCCTCCAGCACGAGCAGTAATGGCACAGGTGTTGTGTCATTT  
TACTCAGTAGCCTCTGGGTTATTTTTAGTTTTCCTTGTTGTTTTTAGCTTTTCCCAT  
TTTAACCTTAAGTGGTATTTCTTGTTAAATATTTATTATGACCATATTATTATCCCTAG  
AGCCACATGGCTTGGGGTCCACCTGCCTGGGTCCGCCCCATCCCTGCCCCCTCTGGCTG  
TCTGACCTGGCCTGGTGACTTCTCTTCTCTGCTCATCTCTCTCCCTGCCTGAGTGGGCAA  
[G, C]  
AGTACAGCCTCACAGAGTGGTGGGATTGTGTGAGATGCCACAGGGAAGCACATGTCAGTT  
GTTGTCACTGTGTAGAACAATGAGTCCCGGATGTGGCCCGCAGGGGAGCAATGGTGACTT  
AATCGCGGGCTTCCTCTGCATTTCCTTTGGTGACTTCCAAGCTAGAACATTCTTTTTTGT  
TTATTTGTTTGAAGCAGGGTCTCACTCTGTTACCTAGGCTGGAGTGCAGTAGCAAAATCA  
TGGCTCACCACAGTCTCAAACCTCCGGGCTCAAGCAATCCTCCACCTCAGCCTCCTGAG

27736 TTCCCCATTTTAACCTTAAGTGGTATTTTCTTGTTAAATATTTATTATGACCATATTAT  
ATTCCCTAGAGCCACATGGCTTGGGGTCCACCTGCCTGGGTCCGCCCCATCCCTGCCCC  
TTCTGGCTGTCTGACCTGGCTGGTGACTTCTCTTCTCTGCTCATCTCTCTCCCTGCCTG  
AGTGGGCAAGAGTACAGCCTCACAGAGTGGTGGGATTGTGTGAGATGCCACAGGGAAGCA  
CATGTCAGTTGTTGTCACTGTGTAGAACAATGAGTCCCGGATGTGGCCCGCAGGGGAGCA  
[A, G]  
TGGTGACTTAATCGCGGGCTTCCTCTGCATTTCCTTTGGTGACTTCCAAGCTAGAACATT  
TTTTTTTGTGTTATTTGTTTGAAGCAGGGTCTCACTCTGTTACCTAGGCTGGAGTGCAGTA  
GCAAAATCATGGCTCACCACAGTCTCAAACCTCCGGGCTCAAGCAATCCTCCACCTCAG  
CCTCCTGAGTAGCTGGGACTACAGGTGCATACCATCACCTGTGGCTAATTTTTTAAATGT  
TTTGATTTTTTTAAATGTTGCTCAGGCTGGTCTTGAAGTGTGGGCTCAAGCAATCCTCC

30688 TACGCAATTGATTTTGTACTGATCTCATAGCTAGACAATTTTGCTAAACTTTTAAAAA  
ATTTATGTACTTTATCTTTTATAGCAGCTTTAAATTTACAGAAAATTTGAGTGAAGATG  
CAGTGTTCCTTAAAGCCGCTAACTCCTCGCACCTTCCCTCAAGTTTCCCCAGTACTAAC  
ATCTTGCAATCAAGTGGTGGCTTTGCAACATTATATAAATTATATCGTCCAGAGTCCATT  
GTTTACATTACGCTTCCTCTCATGTTGTTTCTGTGGTTTACAGATGTGTGATGCA  
[T, C]  
GTGCCCACCACTGCAGTGTACACAGGATCTCACTGCCCCGGAGTCCCTCTGCGCTGTCCC  
CGCCTCCAGAACCCCTTAGTAGCAAACACTGATATTTTACTGTCTCCATAGTTTGCCT  
TTTCAGACTGACCTATTTTCACTTAGTAAGAAGCATTAAAGATTCTTGAGTCTCTTTCTAT  
GGCTCAATAGCACATTTCTTTTAGTGCTGAATAATATTCCATTGTCTGGATGTACCACA  
GTTTATTCACTACCTACTAAGGTGAATGCTTGTCTTCCAAGTTTGGCAACTATG

31172 TCAATAGCACATTTCTTTTGTAGTCTGAATAATATTCCATTGTCTGGATGTACCACAGTT  
TATTCATTACCTACTAAGGTGAATGTCTTGCTTGCTTCCAAGTTTGGCAACTATGAAT  
AAAGTTGCTATCAATGTTAGCGTGCACATAAGTTTTCAGCTCATTTGGGTAAATGCCAAG  
AAGCATGATTGCGGGATCCCTATGGTAAGAGTGTGTTTAGTTCTGTAAGAAGCTGCCAAAC  
TGTATCTTAAGTGGCTGCACCATTTGCGTTTCCACCAGCAATGATGAGCGTTTGTGTCT  
[C, T]  
CACATCCTCACCAGCATTTGCTGTTGTGTTTTGGGTTTTAGCCTTTCTAAGAGGTGTGTA  
GTGGTATCTCCTTGTTTCAATTTGCAATTCCTTAATGACATTATGTTAAATCTTGTCTAT  
ATAGTTATTTGCCATCTGTGTATCTTTTTCAGTGATGTGTCTTTAAAGTCTTTGGCTCA  
TTTTTAAATTTTCTTATTTGTTGAGTTTGTAGTTCTTCATATATTTTGGCTGCCAGT  
CCTTTATCAGATATGTCTTTCGCAAAATATTTTCTGCCTGTGTCTGTCTTTTCTATCTAT

31433 ATTTGCGTTTCCACCAGCAATGATGAGCGTTTTGTTGCTCCACATCCTCACCAGCATTTG  
CTGTTGTGTTTTGGGTTTTAGCCTTTCTAAGAGGTGTGTAGTGGTATCTCCTTGTTTCAA  
TTTGCAATTCCTTAATGACATTATGTTAAATCTTGTCTATATAGTTATTTGCCATCTGTG  
TATCTTTTTCAGTGATGTGTCTTTTAAAGTCTTTGGCTCATTTTTTAAATTAATTTTCTT  
ATTGTTGAGTTTGTAGTTCTTCATATATTTTGGCTGCCAGTCCCTTATCAGATATGTCTTT  
[C, T]

FIGURE 3X

GCAAATATTTTCTGCCTGTGTCTTGTCTTTTCATTCTATTAACAGTATCTTTTGCAGAGC  
CAGTTTTTCATTTCAAGGAAGTCCAGCTTATCAATGTTCTCTTTTCATGTATCATGTTTTTG  
GTGTTGTATCTAAAAAGTTACTGCCAAGCCCAAGGGTACCTAGATTTTTTCTGTGTAT  
ATTCTAGGATTTTAAAGTTTTGCATTTTACATCTAGGTCCATGATTCATTTTGAGTTAA  
CTTTTGTGAAGGGTTATGGTTTGTGTCTAGATTTTTTTTTTTTTTTTTTTTGCATGT

32660 CTCTGGGCTTAAGGAATCCTCCTGTCTCAGCCTCCTGAGCAGCTAGGACCACAGGCATG  
TGCCACTACGTTTCAGCTAATTTTTCAATTTTTTGTAGAGATGGGATCTTGCTCTGTGTC  
CCAGGCTGGTCTCAAACCTCCGCTGCTTTGAGATGATTATATATTTGTGTCTTTGTTA  
ATTTAGAGGATTAATATGGATTTTCTAATGTTAAGACACCTTTGTATTTCTGAGATCGA  
CCTTAGTATTGGTCTATATTTAAGACAGTATTCAGTTTCTCAGTTGTTTTTGTTTTTTG  
[G, T]  
TTTTTTTTTTTGGAGACAGAGTCTCTGTCTCCCAGGCTGGAGTCCAGTGGCACAATCTCAG  
CTCACCGCAAGCTCTGCCTCCCGGATTACAGCCATTCTCCTGCCTCAGCCTCCCGAGTAG  
CTGGGACTACAGGCGCCTGTCTCATGCCCAGCTAATTTTTTGTATTTTGTAGTAGAGACG  
GGTTTTCACCATGTTAGCCAGGGTGGTCTCAATCTCCTGACCTCGTGATCTGCCCACCTC  
GATCTCCCAAAGTGCTGGGATTACAAGGCGTGAGCCACTGCGCCCGGCAGCAGTTTCTCA

32981 TCTCTGTCTCCCAGGCTGGAGTCCAGTGGCACAATCTCAGCTCACCGCAAGCTCTGCCTC  
CCGGATTACAGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCGCCTGT  
CATCATGCCCAGCTAATTTTTTGTATTTTGTAGTAGAGACGGGGTTTACCATGTTAGCCA  
GGGTGGTCTCAATCTCCTGACCTCGTGATCTGCCCACCTCGATCTCCCAAAGTGCTGGGA  
TTACAAGGCGTGAGCCACTGCGCCCGGCAGCAGTTTCTCAGTTTTAATTTGGAGTTTTCG  
[A, C]  
TCTGTGTTTCATGAGTGAGCCTGAAATTTTCACTTTTCCATATCTTATTTCTCTGGGTTC  
TAGAATGAGCTAGAGAGTGTTCCCTCTTCTGTTCTCTGGAAGAGTTGTGTGAGATTAG  
AATGAGTGTGTCTGATAATTTAGTTGCATTCAATTTATAAAATTCCTAGGCCTAGAGTTTT  
TTTTCTGGGAAAAGTTTACATTTTGAATCTATTTTGTAGTAGTTTGTAGACTGTTTAGGT  
TCTCTATTTCTTGATTGAGCCAGTTTGTATAAGTTAATCTTTCTAATTTGTAGATATTTT

33557 AATCTTTCTAATTTGTAGATATTTTCTCTAAGTTTGCAAATGTAATACATAAAACTTTCT  
TGTCATTTCTCACCATATCTGTAGTTCTATCTTTTATTGCTAATATTACTAATTTGTAC  
TTTGACTATTTGTATTTGTTACCTGTTGCCGAGTAACAATATTAGTACAAACCTAGTGGC  
TTAGAACAACACACATTGATTACTTCACCGTTTCTGTGTGTCTGAGAAGTCCAGGCGCGGCC  
TCGCAGGTCGTCTCTGCCTCAGGCTCTCTCCGGGCTTCAGTCAGGGTGTTAGCCAGGAC  
[T, C]  
GGGGTCTCGCCTGAGCTTCCAGTGAGGAAGGATCTGCCTCTGAGCACACAGGGTCTCTCGG  
CAGCATCCCATTCTCAGCTGGAAGCTGCCGACTGCCGTCTGCTGCGGGGCTCTCTAGTA  
TGGCATCTTTCACAAAAGCGAGAAGGGAGAGTTGGTAGAGGGAGTCTGCTAGCACCATTGGG  
AGTCGCGGTACACACAGACCTCGGTCCAGGACCGGCACCCATCAACCTGCGGTGATCTG  
CTGGTTAAAGACAAGTCCCACGTCCACAGGGTGACACTGGAGTAGACACTTCGCTCTGG

33652 TATTGCTAATATTACTAATTTGTACTTTGACTATTTGTATTTGTTACCTGTTGCCGAGTA  
ACAATATTAGTACAAACCTAGTGGCTTAGAACAACACACATTGATTACTTCACCGTTTCT  
GTGTGTCAGAAGTCCAGGCGCGGCTCGCAGGTCGTCTCTGCCTCAGGGTCTCTCCGGG  
CTTCAGTCAGGGTGTAGCCAGGACCGGGTCTCGCTGAGCTTCCAGTGAGGAAGGATC  
TGCTCTGAGCACACAGGGTCTCGGCACGATCCCATTCCTCAGCTGGAAGCTGCCGACT  
[G, A]  
CCGTCTGCTGCGGGGCTCTCTAGATGGCATCTTCACAAAAGCGAGAAGGGAGAGTTGGT  
AGAGGGAGTCTGCTAGCACCATTGGGAGTCGCGGTACACAGACCTCGGTCCCAGGACCCG  
CACCCATCAACCTGCGGTGATCTGCTGGTTAAAGACAAGTCCCACGTCCCACAGGGTGA  
CACTGGAGTAGACACTTCGCTCTGGCTTTTTCAGAGAAGTGGTTATTTTTTGGAAATATC  
AGTTAGATGTAGGATGGGTCTTGTCTTCTAAATCTATTGTTTTCTCTAATTGATTTTT

34390 CTCTGCCAATCCGCTTCCCCTCTGGTGTCTGTGGTTGCTTCTTTTTAAACCCCTCATC  
GGTCTGTGTAAACTGTTTATTTTTATGTGGTTTTTAAGGGAGACCATCTCATTCTTTTG  
AGACCTTGAAAGGATGGAATTGGGATAGGTAACTGCTGTTTTTACCAGAATGTTCACTG  
GACCAATCTCGTGTTCAGGGAGACCTCACGCAGGGCTTAGAGTTCTGTCGGCGGCAGC  
AGAGGGCCGATGGCTCCTGGGAAGGGTGAGTGAGCCTCCACTCGTGAGTGACAGAGATGCA  
[T, C]

FIGURE 3Y



36001

FIGURE 3Z

TGCAGAGTGCCAGTCCCAGATCCATAACACATGCTGGGCCATGATGGGGCTGATGGCCG  
TTCCGTGGGGACGACGGGACCGTCCCTGAGCCTTGGGTTTGGGTAGAGGAGGGACACTCA  
GCTGTGAGCCGGTGGCTGGGCTGAGTGAATGTAGAGAGGAGGGGAGGCCTGTGGGCCAG  
GTCAGCTGCCACTCTGGGAACAGACACCTACAAGAGCCACATGCCCTGGTTCTTGGGGCAA  
GAACGTGGGCTGCTCTGACCAAGTGGGGCCCTGCAGAGAGGCTCGCCTCTTAGAAGTGAA

38948 ACAGCTCCCCAATGGCGACTGGCCGAGGTATGCCGCCAGGGACCTGAGCGCACAAAGGCC  
CAGCACTGACCTCCAGCGTGCATGGCTGTTTCCACGTCCCCCTGCTCTGTGTCTTTTGTG  
GGGTACTTTGGACACTTGGGAGGCGTCACCTCTGCCAGTGAATGCCACAGTTGGTGGCAG  
GTCTGTGGCAGGTGGTCGGGTCTTAAAGTCCAGATCTTGCTGTGTGTTCAAGTGATGCTC  
TGGGTGGGGGAGGAGCTGGATGGGAGAAGCCAGTGGGCGGAAGCCTTTTGTGTCAGGA  
[C, T]  
AGACCCCTCCCACTCCAGATGACCTAGTGGCCCCTCACTGAGCCAGAAGTCCCTGTGGTGT  
GGGTGTCATGAGGTGATGTGAGGCCAACCGCCCTCCCTGGGATGAGGCTGAGTTGGTGG  
AAGCTGATGTGGTTGTGAGGGGCTGGTGACCTGGCTTAGGGTTTGTGTCAGGGCGGGGA  
GTCTGAGCTGGGCTGATGGTGCCATGACTGATGCGGGATGGACTACTTGCTTTCCATATGC  
TCTTGCTTAATTAGCCCTTTCCAGGCTGACTACCCACAAGCCAGCCAAGCCAACAGCCA

39160 GATCTTGCTGTTGTTTCAAGTGATGCTCTGGGTGGGGGAGGAGCTGGATGGGAGAAGCCA  
GTGGGCGGGAAGCCTTTTGTGTCAGGACAGACCCCTCCCACTCCAGATGACCTAGTGCC  
CCTCACTGAGCCAGAAGTCCCTGTGGTGTGGGTGTCATGAGGTGATGTGAGGCCAACCGC  
CCTCCCTTGGGATGAGGCTGAGTTGGTGAAGCTGATGTGGTTGTGAGGGGCTGGTGACC  
CTGGCTTAGGGTTTGTCTGCAGGGCGGGAGTCTGAGCTGGGCTGATGGTGCCATGACTGA  
[T, C]  
GCGGATGGACTACTTGCTTTCCATGCTCTTGCTTAATTAGCCCTTTCCAGGCTGACTC  
ACCCACAAGCCAGCCAAGCCAACAGCCAGGGCTCCAGTTAGGGACTAGCCCTCAGCTGA  
CTGGTGAAGCCTTTGTGTTTATTTCTCTGTGTTCTTTTAGGAAAACATTGCTGGGGTCTT  
CAACAAGTCTGTGCCATCTCCTACACGAGCTACAGGAACATCTTCCCATCTGGGCCCT  
CGGCGCTTCTCCAGCTGTACCTGAGAGAGCCCTTGCTGGCCACCCTGAGAATATGC

40405 TGTCATGGAGCCGCATACCCCTGGGTGTGAGCTCGCCTGCATATGCAGGGTCTGTCTATG  
GAACATCCCAAGTCTGTGACGAGGGGAGCCCCATGCCCTGGGACATGAACCCACCTGC  
GTGGAATGCTGTTTGTGAGGTGTCTACAGGGTTTATAGTAGTCTTGTGGACACAGAAATG  
CACAGGGGACACTTACGGACACAGAAATGCACAGGGGAGGCCGAGCATAACCAGGGGTGA  
GGGCGAGGCAGCAGTTGTAGTTACTGCCGCGGGGCACTGCTATGTGACGGGACAGCCAGC  
[G, A]  
CCCAGCCCATCACTCCCTGGGCTGGCTGGCAGGTATGGCACCCCTGGGAGCCCGGCAT  
ATACCCAGGGCACCCCTACGGCTGCCGCCAGTCTCATGCCAGGTGGGTGCTCTGGGCTG  
GAGCGAGGGCCAGGTTTTGGGCCGAGGCTTCCCAGGCAATCCTGTGAGCTCCCTCTAG  
CCTCTGACCCAGTCTGGTCTGGCTTGCATGGATGTAGGGCTTGGGGTGGGAAGTTACAGT  
CCTGGCTTTGCCCTTTCCTGATGTGGATGAGCAGCTCACATGCTCAGGGCCACCTGAGAC

40794 CAGTCTCATGCCCAGGTGGGTGCTCTGGGCTGGAGCGAGGGCCAGGTTTGGGCCGAGGC  
TTCCCCAGGCAATCCTGTGAGCTCCCTTCTAGCCTCTGACCCAGTCTGGTCTGGCTTGCA  
TGGATGTAGGGCTTGGGGTGGGAAGTTCAGGTCCAGGCTTGGCTTTGCCCTGATGTGGAT  
GAGCAGCTCACATGCTCAGGGCCACCTGAGACTGTCACTGCTCTCCCTGGCTACTGGGA  
GGAGTCACTGAGAGCTTCGTTACCCCTGCTGCCTTGCCAGGGCACACCCCTATACCTCCT  
[C, T]  
ATCTGCTCTTCCCTCCCTGCCGCTTCTGGGCAGGTAGCAGTCCCTGGCCTCTCCCTCT  
GGCTGATCACTCTCCCTCAGGCAGTGGAGATCTGCGTCTGGACACCCCTCAGATCCTGTCA  
TTGCTTGGCCAGAGTCTTTCAGGGCACCCCTCTGCTTGGTGTGCGGTCCAGGGCTCTC  
ATCCAGGTGCCGCACCCCTCTGGGCTTCTGTGTCAGCTTCCCTTGCCCATGTGCTGTAC  
TGACTCTCCTTGGGACTCGCCTGCCTGCTCAGAGCCCTGCAGGGCTTGGTCTGAGTGCCTG

40961 GCCTGATGTGGATGAGCAGCTCACATGCTCAGGGCCACCTGAGACTGTCACTGCTCTCCC  
CTGGCTACTGGGAGGAGTCACTGAGAGCTTCGTTACCCCTGCTGCCCTTGCCAGGGCACA  
CCCTATACCTCCTCATCTGCTCTTCCCTCCCTGCCGCTTCTGGGCAGGTAGCAGTCCC  
TGGCTCTCCCCCTGGCTGATCACTCTCCCTCAGGCAGTGGAGATCTGCGTCTGGACACC  
CTCAGATCCTGTCAATTGCCCTGCCAGAGTCTTTCAGGGGCACCCCTTGCCTTGGTGTGC  
[A, G]

FIGURE 3AA

GTCCAGGGCTCTCAGGAGGTCGCGACCCCTCTGGGGTCTTCTGTCCAGCTCCCTTGCCC  
CATGTGCTGTCACTGACTCTCCTTGGGACTCGCCTGCCTGCTCAGAGCCCTGCAGGGCTT  
GGTCAGCTGCCGTGTTCACTGTCAACACTTCCCTGCACATCTTAAACTGGGCTTTATTTT  
CGCTGAAGGAACGTGTTGGGACCCCTTGACATCTGTACAGGTTTGCACATGCTGTTTTTTT  
TTCTCAGCCCACGTGTTCTCCCCACGTGGGGTAGCAGCAGGACAGACAGTGAATCACAG

41891 AGGGAAAACAGATATTTTAAGAGATAATAGCATAGCCTATTTTAATATGTTTTAAAGGCC  
ATAAGCATATCCAGGAAGATAAATAAACGTGATACAATGTCCACATAGGAGGAACTTTCT  
TTCCTGCTGCTGTTTTTCCTTACAGTGGCCTTCAAGTCACAGGACGACGCGATTCCCTGC  
CCTCTTCGGTGTTATTACACAGGCAGGACTTCAGTGTGAGTATCCCTGCCTTCAGTCTTC  
TTTAGAAATCACATCTGTGTTCAATCCATTGTTTAGAGGGAGTGTATTTTTCCTGTTCCA  
[C, T]  
GAAGAGGACTTTTTGTTTCAACAATTGGATCACAATGCAGAGGAGTCTGTTCCCTCCCCCGTC  
GGCTTCTCGGTGCTGGGAGGGTGACCTGTCCAGATGACTCATCACCTGACATGCTCTT  
GACAAAGGACACCACCAAGAGGAGATGGCAGCTGTACCGGTGCAGCCTCTGTCTGAGGGG  
GATATTTGCCTCAGTGTGATTAAAAATCAGTCATGAAAGATTTTGAATTCAGATTATTT  
TTATCAGGAACAGATTTTGAACATCCTGAAATCTTTTCCCTGGCATCATATTAGGTTTTTC

FIGURE 3BB